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(54) Title: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION		
SEQ ID NO: 5    rAIF-1 MSQSKDLGGKAFGLLKAQQEERLDGINKHFLDDPKYSSDEDLQSKEAF 50    ..       ..... :::   ...    SEQ ID NO: 42   hAIF-1 MSQTRDLOGGKAFGLLKAQQEERLDEINKQFLDDPKYSSDEDLPKLEGF 50    ..       ..... :::   ...    rAIF-1 KTKYMEFDLNGNGDIDIMSLKRMLEKLGVPRTHLEKKLIREVSSGSEET 100  ..       ..... :::   ...    hAIF-1 KEKYMEFDLNGNGDIDIMSLKRMLEKLGVPRTHLEKKLIGEVSSSGSET 100  rAIF-1 FSYSDFLRMLGKRSAILRMILMYEEKNEHQKPTGPAPAKAISLP 147    ..       ..... :::   ...    hAIF-1 FSYPDFLRMLGKRSAILKMILMYEEKAREKEKPTGPAPAKAISLP 147		
(57) Abstract  Differentially expressed allograft genes, methods of screening therefor, and methods of diagnosing and treating allograft rejection and other conditions related to vascular inflammation, such as atherosclerosis. The figure is a comparison between rat and human AIF-1 amino acid sequences.		

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### MEDIATORS OF CHRONIC ALLOGRAFT REJECTION

This application is a continuation-in-part of  
5 copending application serial number 08/171,385, filed  
December 21, 1993.

#### Statement as to Federally Sponsored Research

This invention was made with U.S. Government  
support under HL43318 awarded by the National Institutes  
10 of Health. The U.S. Government therefore has certain  
rights in the invention.

#### Background of the Invention

The invention relates to tissue and organ  
transplantation.

15 The major limitation to long-term survival after  
organ transplantation in humans is the development of  
chronic rejection. Cardiac transplantation, for example,  
is frequently characterized by an obliterative  
arteriosclerosis with progressive thickening of the  
20 interior of the blood vessel that eventually results in  
ischemic injury (Schoen, F.J. and P. Libby, 1991, Cardiac  
Transplant Graft Arteriosclerosis, *Trends Cardiovasc.*  
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J.P. Scott, E. Solis, T.A. English, S.R. Large, P.M.  
25 Schofield, and J. Wallwork, 1991, Risk factor analysis  
for the major hazards following heart  
transplantation-rejection, infection, and coronary  
occlusive disease, *Transplantation*, 52:244-252; Cramer,  
D.V., 1993, Graft Arteriosclerosis in Heart  
30 Transplantation, R. G. Landes Company, Austin, TX).  
Studies of vessels from human heart transplant recipients  
have revealed an intimal hyperplasia that is concentric  
and diffuse, involves a spectrum of vessels, and is

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highly prevalent. Animal models have shown that in the first stage of arteriosclerotic thickening, monocytes/macrophages accumulate. In the intermediate stage, macrophages and smooth muscle cells both  
5 accumulate, and in the later more obliterative stage, smooth muscle cells predominate.

Chronic transplant rejection is likely to be a complex process mediated by a spectrum of factors which have been difficult to eliminate. Transplant  
10 arteriosclerosis occurs only in the donor heart and spares the host vessels. One hypothesis about the arteriosclerotic process holds that a chronic, cell-mediated immune response to alloantigens produces cytokines that mediate neointimal smooth muscle cell  
15 accumulation in the graft-derived vasculature, in a manner analogous to the process of delayed-type hypersensitivity (Schoen et al., supra), but little is known about factors that regulate the specific  
20 localization or function of mononuclear cells in the interstitium and vessels of cardiac allografts. The pathogenesis of transplant arteriosclerosis is unknown, and studies to elucidate the process have been limited by difficulty in obtaining useful clinical specimens.

#### Summary of the Invention

25 The invention addresses these problems by providing methods to identify genes which are differentially expressed in allograft tissue undergoing rejection, to diagnose chronic rejection, and to treat patients undergoing transplant rejection. Furthermore,  
30 factors identified in association with chronic rejection also appear to play a role in other forms of arteriosclerosis.

As an alternative to conventional transcriptional analysis of selected known factors that could be involved

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in chronic rejection, screening assays which utilize a modification of the differential mRNA display technique were developed to identify potential mediators that are novel or have not been previously implicated in chronic rejection.

In one aspect, the invention features a method of identifying a gene which is differentially expressed in an allograft of a given tissue type compared to a syngraft of the same tissue type, by obtaining mRNA from the allografts and syngrafts, and determining whether the quantity of an allograft cDNA or transcript is increased or decreased compared to that of the corresponding syngraft transcript. An increase in the amount of a given transcript in tissue from an allograft compared to the amount of the corresponding transcript in corresponding tissue from a syngraft indicates that the given transcript encodes a mediator of allograft rejection. The term "differentially expressed" refers to a given allograft gene transcript, and is defined as an amount which is substantially greater or less than the amount of the corresponding syngraft transcript. By the term "gene transcript" is meant a mRNA or cDNA.

In one embodiment, the amount of allograft transcript is at least four times the amount of the corresponding syngraft transcript; preferably, the amount of syngraft transcript is absent or undetectable.

In another aspect, the invention features a method of diagnosing (1) allograft rejection, or (2) pre-atherosclerotic vascular inflammation and/or vascular injury, by detecting an increase in expression of a differentially expressed allograft gene at the site of the rejection, inflammation, or injury. Detection of increased expression of genes previously identified using the screening assays of the invention, such as allograft inflammatory factor-1 (AIF-1), allograft inflammatory

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factor-2 (AIF-2), ubiquitin, P1, or galactose/N-acetylgalactosamine (Gal/GalNAc) macrophage lectin, can be used to diagnose transplant rejection in a patient. Detection of expression of these genes can be

5 accomplished by measuring gene transcripts, e.g., mRNA or cDNA, using standard techniques such as differential display mRNA analysis, polymerase chain reaction (PCR), *in situ* hybridization, or Northern blotting techniques, or by measuring the polypeptide product using known  
10 methods, such as Western blotting techniques, fluorescein-activated cell sorting (FACS), immunohistochemistry, immunoassays, or non-invasive imaging.

The invention also features an isolated DNA which  
15 encodes AIF-1, e.g., rat AIF-1 cDNA (SEQ ID NO:4) or human AIF-1 cDNA (SEQ ID NO:43). An isolated DNA which hybridizes at high stringency to a 20 nucleotide fragment of SEQ ID NO: 1, 4, or 43; and an isolated DNA which encodes an AIF-1 polypeptide, e.g., rat AIF-1 polypeptide  
20 (SEQ ID NO:5) or human AIF-1 polypeptide (SEQ ID NO:42), are also included. A substantially pure preparation of an AIF-1 polypeptide is also included. The DNA of the invention preferably encodes a mammalian AIF-1 polypeptide or functional fragment or isoform thereof,  
25 and most preferably encodes a rat or a human AIF-1 polypeptide.

Also within the invention is an isolated DNA which encodes AIF-2 polypeptide, or a functional or antigenic fragment thereof. Such a DNA may include the sequence of  
30 SEQ ID NO: 2, 3, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17,  
18, 19, 20, 21, 22, 23, 24, 25, 26, or 27; or may be an isolated DNA which hybridizes at high stringency to a DNA containing such a sequence. A substantially pure preparation of a polypeptide containing a sequence  
35 encoded by the DNA of SEQ ID NO: 2, 3, 8, 9, 10, 11, 12,

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13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26,  
or 27 is also within the invention. The DNA of the  
invention preferably encodes a mammalian AIF-2  
polypeptide or functional fragment or isoform thereof,  
5 and most preferably encodes a rat or a human AIF-2  
polypeptide. The invention encompasses isolated DNA  
containing part or all of the sequence of either AIF-1 or  
AIF-2. Also included are vectors containing the isolated  
DNA; cells, which can be prokaryotic or eukaryotic,  
10 containing the isolated DNA or vector; and methods of  
manufacturing recombinant AIF-1 or AIF-2, such as methods  
of culturing the cells containing isolated DNA of the  
invention under conditions permitting expression of the  
DNA. An "isolated DNA", as used herein, refers to a  
15 given DNA sequence which may be single stranded or double  
stranded, sense or antisense, and which has been removed  
from the sequences which flank it in a naturally  
occurring state, i.e., the sequences adjacent to the  
given DNA sequence in a genome in which it naturally  
20 occurs. The term includes, for example, a recombinant  
DNA which is incorporated into a vector, into an  
autonomously replicating plasmid or virus, or into the  
genomic DNA of a prokaryote or eukaryote; or which exists  
as a separate molecule (e.g., a cDNA or a genomic DNA  
25 fragment produced by PCR or restriction endonuclease  
treatment) independent of other DNA sequences. As used  
herein, the term "substantially pure" describes a  
compound, e.g., a polypeptide, which has been separated  
from components which naturally accompany it. Typically,  
30 a polypeptide is substantially pure when at least 10%,  
more preferably at least 20%, more preferably at least  
50%, more preferably at least 75%, more preferably at  
least 90%, and most preferably at least 99% of the total  
material by dry weight in a sample is the polypeptide of  
35 interest. Purity can be measured by any appropriate

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method, e.g., polyacrylamide gel electrophoresis, column chromatography, or HPLC analysis. By the term "high stringency" is meant DNA hybridization and wash conditions characterized by relatively high temperature and low salt concentration, e.g., conditions described in Sambrook et al., 1989, *Molecular Cloning: a Laboratory Manual*, second edition, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., e.g.,  $0.2 \times \text{SSC}$ ,  $0.1\%$  SDS at  $60^\circ\text{C}$  wash conditions.

10 In another aspect, the invention features a method of inhibiting (1) rejection of a transplanted tissue in an animal, or (2) atherosclerotic plaque formation at the site of vascular inflammation or injury, by introducing into the animal a compound which inhibits expression of a  
15 differentially expressed allograft factor that is upregulated during rejection of an allograft. An example of such a compound is an antisense DNA fragment complementary to the coding sequence or promoter of a differentially expressed allograft gene, e.g., Gal/GalNAc  
20 macrophage lectin, AIF-1, AIF-2, ubiquitin, or P1. Alternatively, rejection or other inflammatory processes could be inhibited by exploiting the differentially expressed factor as a means of targeting and killing cells which bear the factor on their surface. A  
25 recombinant or chemically conjugated hybrid toxin in which a toxic moiety (e.g., an enzymatically active fragment of diphtheria toxin or ricin, or a cytotoxic radioisotope) is linked to a ligand or antibody specific for the differentially expressed factor. The Gal/GalNAc  
30 ~~macrophage lectin is an example of such a factor~~ expressed on the surface of cells to be targeted by this method.

The invention also features a method of inhibiting (1) rejection of a transplanted tissue, or (2) formation  
35 of atherosclerotic plaques at the site of vascular



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inflammation or injury in an animal, by introducing into the animal a compound which inhibits binding of a cell-associated lectin to a carbohydrate ligand on the allograft. In preferred embodiments, the lectin is

5 Gal/GalNAc macrophage lectin, and/or is present on the surface of a macrophage. The invention also includes compounds which inhibit binding of the lectin to its carbohydrate ligand, such as Gal/GalNAc macrophage lectin-specific antibody, a polypeptide which binds to

10 Gal/GalNAc, a carbohydrate or compound containing a carbohydrate which binds to Gal/GalNAc macrophage lectin, or a compound containing a soluble carbohydrate-binding fragment of Gal/GalNAc macrophage lectin, all of which may be formulated in a pharmaceutical excipient for

15 administration to animals.

In another aspect, the invention includes a screening assay to identify a candidate compound capable of inhibiting allograft rejection and/or atherosclerotic plaque formation, by contacting Gal/GalNAc macrophage

20 lectin with its carbohydrate ligand in the presence and absence of a candidate compound, and measuring binding of the lectin to its carbohydrate ligand. A decrease in binding in the presence of a candidate compound compared to the level of binding in the absence of the candidate

25 compound is an indication that the candidate compound inhibits allograft rejection and/or atherosclerotic plaque formation. This screening method may be carried out *in vitro* as well as *in vivo*.

Other features and advantages of the invention

30 will be apparent from the following detailed description and other embodiments of the invention, and from the claims.

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Brief Description of the Drawings

Fig. 1A is a photograph of a differential mRNA display gel showing an upregulated PCR fragment in chronically rejecting hearts produced by allogeneic cardiac transplantation. The 6% polyacrylamide gel electrophoretic analysis of randomly amplified PCR products shows a cDNA fragment identified in the 4 heart samples obtained after allogeneic transplantation (allografts) but not in the 2 hearts obtained after syngeneic transplantation (syngrafts).

Fig. 1B is a photograph of a Northern blot. The upregulated PCR fragment was harvested and reamplified from the differential display gel shown in Fig. 1A. When radiolabeled with  $^{32}\text{P}$  and used as a probe in Northern analysis, the fragment hybridized to 1.4-kb transcripts found only in the 4 lanes containing the hearts subjected to allogeneic transplantation, which develop chronic rejection (lanes 3-6), but not to the 2 hearts from syngeneic cardiac transplantation (lanes 1 and 2). Samples from the same total RNA extraction were used in both the PCR and Northern analyses.

Fig. 1C is a photograph of a RNA gel stained with ethidium bromide before transfer to a fiber membrane, to demonstrate that 20  $\mu\text{g}$  of total RNA was loaded into each lane.

Fig. 2A is a photograph of a Northern blot analysis showing upregulation of transcripts in an expanded series of 7- and 14-day cardiac allografts, but not in paired host hearts. Northern blot analysis using the transplanted heart (cardiac allograft) and host heart (exposed to the same circulation but histologically normal) from an additional 2 syngeneic and 6 allogeneic cardiac transplantations confirmed and extended the allograft-specific induction patterns. PCR-amplified DNA fragment from the differential display study hybridized

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to 1.4-kb transcripts found only in allogeneic transplanted hearts harvested at 7 and 14 days (lanes 5-7 and 14-16) but not to transcripts from the paired host hearts or syngeneic transplanted hearts.

5           Fig. 2B is a photograph of a RNA gel stained with ethidium bromide before transfer, to demonstrate that 20  $\mu$ g of total RNA was loaded into each lane (with the exception of lane 11).

          Fig. 3A is a photograph of a Northern blot  
10 analysis of RNA from rat organs using the full-length Gal/GalNAc macrophage lectin cDNA as a probe. Tissue-specific upregulation was observed in cardiac allografts. The full-length cDNA was isolated from a rat cardiac allograft cDNA library and used as a probe in Northern  
15 blot analysis completed with 20  $\mu$ g/lane total RNA from the indicated organs. The cDNA probe hybridized strongly to 1.4-kb transcripts in the 28-day cardiac allograft sample. In contrast, hybridization levels were low in all other organs examined, including those rich in  
20 resident monocytes and macrophages. To examine possible changes in expression related to systemic effects of inflammatory stimulation, the paired host spleen and a spleen harvested 8 hours following intraperitoneal lipopolysaccharide injection were included.

25           Fig. 3B is a photograph of a RNA gel stained with ethidium bromide before transfer, to demonstrate that each lane contains 20  $\mu$ g of total RNA.

          Fig. 4A is a graph of the linear range of Gal/GalNAc macrophage lectin reverse transcription-PCR  
30 assay. Rat cardiac allograft cDNA was amplified using specific Gal/GalNAc macrophage lectin primers and separated electrophoretically on 1% agarose gels.

<sup>32</sup>P incorporation in the PCR product band from dried gels was measured in PhosphorImager units. The  
35 linear relationship between amplified Gal/GalNAc

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macrophage lectin product bands and PCR cycle identifies the assay range where amplified product is proportional to the initial target mRNA.

Fig. 4B is a graph showing the linear relationship between amplified Gal/GalNac macrophage lectin product bands and added cDNA (represented as the calculated amount of total RNA in the PCR reaction, lower panel) which identifies the assay range where amplified product is proportional to the initial target mRNA.

Fig. 5 is a bar graph showing a time course of Gal/GalNac macrophage lectin gene expression after allogeneic cardiac transplantation. Corrected levels were derived by normalizing Gal/GalNac macrophage lectin PCR values against those for the control gene, Glyceraldehyde 3 phosphate dehydrogenase (G3PDH), and are shown in relative units. There was a significant increase in cardiac transplant (or allograft) cDNA at 7, 14, 28, and 75 days (black bars) following transplantation compared with cDNA from the day-0 heart (harvested but not transplanted), paired host hearts (hatched bars), and a 14-day syngraft (stippled bar) ( $P < 0.008$ ). Data are plotted as means  $\pm$  SEM and represent 4 separate PCR analyses.

Fig. 6 is a bar graph showing upregulation of Gal/GalNac macrophage lectin transcripts localized within the allografted heart. PCR analysis to identify relative differences in Gal/GalNac macrophage lectin transcript levels was performed on a set of cDNAs that included the transplanted heart (black bars) and the matching host heart and spleen (hatched bars) from 2 additional allogeneic cardiac transplantations harvested at 7 and 14 days. Corrected Gal/GalNac macrophage lectin levels were derived by normalizing the lectin PCR band value against that of the G3PDH control value. Gal/GalNac macrophage lectin levels increased significantly in the transplanted

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hearts compared with the host spleens (rich in resident macrophages but not subject to local allogeneic stimulation) and the host hearts normal on histologic examination ( $P < 0.0001$ ). Data are plotted as means  $\pm$  SEM and represent 4 separate PCR analyses.

Fig. 7 is a bar graph showing an increase in Gal/GalNAC transcripts levels in exudative macrophages. Corrected Gal/GalNAC transcript levels were significantly higher in thioglycolate-elicited macrophages ( $P < 0.0001$ ) and cardiac allografts compared with adherent and nonadherent splenocytes even after 4 hours of stimulation with concanavalin A or lipopolysaccharide/interferon- $\gamma$ . Data are plotted as means  $\pm$  SEM and represent 4 separate PCR analyses.

Figs. 8A-8D are photographs of microscopic analyses of cardiac allograft cells showing *in situ* localization of Gal/GalNAC macrophage lectin mRNA. Sections were hybridized to  $^{35}\text{S}$ -labeled antisense (Fig. 8A and Fig. 8B) or sense (Fig. 8C and Fig. 8D) riboprobes. Arrows in lower-power sections (Fig. 8A and Fig. 8C) indicate the regions shown in higher magnification (Fig. 8B and Fig. 8D). Silver grains indicating hybridization of Gal/GalNAC macrophage lectin mRNA are clustered over a subset of inflammatory cells in the interstitium and perivascular spaces (Fig. 8A, 260 $\times$ ). Arrows mark representative positive mononuclear cells that are seen best at higher magnification (Fig. 8B, 600 $\times$ ). Arrowheads mark representative inflammatory cells without hybridization. Little hybridization is visible in adjacent noninflammatory cells such as cardiac myocytes. The sections hybridized with sense riboprobes show no significant hybridization (Fig 8C, 260 $\times$ ) and (Fig. 8D, 600 $\times$ ).

Figs. 9A-9C are photographs of differential display gels comparing RNAs from syngeneic and allogeneic

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hearts. Total RNA was extracted from hearts after syngeneic (Lanes 1 and 2) and allogeneic (Lanes 3-6) transplantation and subjected to differential mRNA display analysis. Autoradiograms of amplified [ $\gamma$ -<sup>35</sup>S]dATP-labeled PCR products (after electrophoresis on 6% polyacrylamide gels) are shown for three different primer combinations (Figs 9A-9C) that identified four distinct fragments (arrows) upregulated in the allogeneic group. Primer combinations included T<sub>12</sub>VC as 3' primer for all reactions and various 5'-primers: Fig. 9A, OPA-16 (AGCCAGCGAA) (SEQ ID NO: 28); Fig. 9B, OPA-04 (AATCGGGCTG) (SEQ ID NO: 29); and Fig. 9C, OPA-14 (TCTGTGCTGG) (SEQ ID NO: 30). Lane 4 in Fig. 9A shows a PCR reaction that failed.

Figs. 10A and 10B are photographs of RNA blot analyses confirming allograft-specific gene induction for Bands 1, 2, 11, and 12 identified initially by differential mRNA display. Total RNA (20  $\mu$ g) obtained from syngeneic (Lanes 1 and 2) or allogeneic (Lanes 3-6) transplantations were hybridized with cDNA probes generated by PCR reamplification of bands recovered from differential display gels (Fig. 10A) or cloned cDNA fragments (Fig. 10B). Arrows indicate allograft-specific hybridization patterns. Arrowheads indicate hybridization in all six lanes (which was considered nonspecific). RNA loading (bottom panel) was evaluated by reprobing the same blot with the rat ribosomal 36B4 homologue.

Fig. 11A is a representation of the nucleotide sequence and deduced amino acid sequence of the rat AIF-1 cDNA (SEQ ID NO: 4). Nucleotide numbering is indicated on the right and amino acid numbering is on the left. The boxed area indicates the region of the EF-hand-like motif (with the conserved loop segment shaded). A putative polyadenylation site is underlined.

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Fig. 11B is a graph showing the AIF-1 hydrophilicity plot generated with the Kyte-Doolittle algorithm. Regions of hydrophilicity are above the center line.

5            Fig. 12 is a genomic Southern analysis showing a representative autoradiogram from a blot hybridized with the <sup>32</sup>P-labeled rat AIF-1 cDNA. Genomic DNA extracted from rat (R), mouse (M), and human (H) tissue samples was digested with the restriction enzymes indicated above the  
10   blots.

            Fig. 13A is a representative autoradiogram from a Northern blot containing total RNA extracted from the indicated rat organs after hybridization with <sup>32</sup>P-labeled AIF-1 cDNA. AIF-1 transcripts of 0.7 kb are visible in  
15   the 28-day cardiac allograft (lane 2), the spleen (lane 3), and the testis (lane 7).

            Fig. 13B is the same RNA gel as in Fig. 13A, stained with ethidium bromide before transfer to demonstrate loading in each lane.

20           Fig. 14 is a graph illustrating the time course of AIF-1 gene expression after allogenic cardiac transplantation. Corrected levels were derived by normalizing AIF-1 <sup>32</sup>P-reverse-transcriptase PCR values against those for the control gene, C3PDH, and are shown  
25   in relative units. Levels increased significantly in cardiac allograft cDNA at 7, 28, and 75 days after transplantation (*hatched bars*) compared with cDNA from paired host hearts (*black bars*) and day-75 syngrafts (*stippled bar*) ( $p < 0.003$ ). Values are shown for a  
30   representative experiment on two transplants per group.

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Data are plotted as means $\pm$ SEM and represent three separate PCR analyses.

            Figs. 15A and 15B are photomicrographs illustrating in situ localization of AIF-1 transcripts in  
35   rat cardiac allografts. Frozen sections were hybridized

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with <sup>35</sup>S-UTP-labeled antisense (Fig. 15A, x300) and sense (Fig. 15B, x300) riboprobes. Silver grains indicating hybridization of AIF-1 mRNA are clustered over mononuclear inflammatory cells in the perivascular  
5 (arrow) and interstitial spaces.

Fig. 16A is a representative autoradiogram of a Northern blot illustrating AIF-1 transcript expression in isolated rat cell populations. The various lanes contain total RNA extracted from cardiac allografts (lanes 1 and  
10 2), spleen (lane 3), bone marrow cells (lane 4), macrophages derived from bone marrow (lane 5), BCG-elicited peritoneal macrophages (lane 6), casein-elicited peritoneal neutrophils (lane 7), T lymphocytes purified from a splenocyte suspension (lane 8), and aortic smooth  
15 muscle cells (lane 9).

Fig. 16B is the same RNA gel stained with ethidium bromide to demonstrate loading.

Fig. 17 is a Western blot analysis of AIF-1 antigen in various cell types. Western blots containing  
20 protein extract from the tissues or cell populations indicated were immunostained with rabbit anti-AIF-1 serum. Chemoluminescent detection shows a band of 17-kD in extracts from a day-28 cardiac allograft (lane 2), spleen (lane 3), and bone marrow-derived macrophages  
25 (lane 5) but not in extracts from a host heart (lane 1), femoral bone marrow cells (lane 4) or unstimulated (lane 6) or Concanavalin A-stimulated T lymphocytes (lane 7).

Figs. 18A-18F are a series of photomicrographs illustrating immunostaining of the AIF-1 antigen in  
30 various tissue sections. Cells showing AIF-1-positive staining in the cytoplasm of a subset of mononuclear cells (Figs. 18A-C) are visible in the interstitium of a 14-day cardiac allograft (Fig. 18A, x940) and in the splenic red pulp (Fig. 18B, x80 and Fig. 18C, x940). No



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staining is visible if the primary antibody is omitted (Figs. 18D-F).

Fig. 19A is a bar graph illustrating the upregulation of AIF-1 transcript levels by IFN- $\gamma$  in vitro. Corrected AIF-1 transcript levels were significantly higher in IFN- $\gamma$ -treated J774A.1 cells ( $p < 0.0001$ ) compared with cells treated with buffer, LPS, combined LPS and IFN- $\gamma$  (L/I) or phorbol 12-myristate-13-acetate (PMA) (24 h).

Fig. 19B is a graph illustrating the time-dependent increase in AIF-1 transcript levels in J774A.1 cells cultured in the presence of 100 units/ml IFN- $\gamma$  for the indicated periods.

Fig. 19C is a graph illustrating the dose-response in J774A.1 cells of IFN- $\gamma$ -induced increases in AIF-1 transcript levels after 24h of stimulation. In each of Figs. 19A-19C, data are plotted as means  $\pm$  SEM and represent three separate PCR analyses.

Figs. 20A and 20B are bar graphs demonstrating that modulation of the allogeneic immune response decreases AIF-1 transcript levels in cardiac allografts. In Fig. 20A, the effect of EFAD diet is illustrated. Corrected AIF-1 transcript levels decreases significantly in day-28 cardiac allografts harvested from rats fed the EFAD diet (*hatched bars*) in comparison with allografts harvested from rats fed a control diet (*black bars*) ( $p < 0.0001$ ). In Fig. 20B, the effect of CTLA-4 Ig treatment is shown. Corrected AIF-1 transcript levels were significantly lower in cardiac allografts harvested at day 75 from rats treated with CTLA-4 Ig (*black bar*) ( $p < 0.0001$ ) in comparison with allografts from control rats (*stippled bar*) or allografts from cyclosporine A-treated animals (*hatched bar*). Administration of CTLA-4 Ig in combination with donor cells further decreased AIF-1 transcripts to a level similar to that observed in

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syngrafts (white bar) ( $p < 0.0001$ ). Data are plotted as means  $\pm$  SEM from two or three transplants per group and represent three separate PCR analyses.

Figs. 21A-C are photographs of gels illustrating the identification of AIF-1 gene transcripts in transplant endomyocardial biopsies. In Figs. 21A and 21B, ethidium-stained agarose gels are shown containing RT-PCR products amplified using primers for AIF-1 (Fig. 21A) and the reference gene, B-2-microglobulin (Fig. 21B). Bands of variable intensity are seen in lanes 2-6 representing endomyocardial biopsies from human heart allografts (lane 2-6) compared with the control cDNA from 28 day rat cardiac allografts. In Fig. 21C, Southern blot analysis of the same products shows hybridization to the lanes (3-6) with a nested human AIF-1  $^{32}\text{P}$  labeled oligonucleotide probe.

Fig. 22 is a comparison between the deduced amino acid sequences for the AIF-1 coding region of rat (upper) (SEQ ID NO: 5) and human (lower) (SEQ ID NO: 42) cDNAs, showing 90% identity (1) and 95% similarity (.or:).

Figs. 23A-D are photomicrographs of human cardiac allograft sections immunostained with anti-rat-AIF-1 antibody (Figs. 23A (low magnification) and 23B (high magnification), or the anti-CD68 antibody (Figs. 23C (low magnification) and 23D (high magnification)). AIF-1 staining localizes to mononuclear cells found within the interstitium and perivascular spaces of cardiac allografts. These mononuclear cells are most likely macrophages, given that in serial sections, cells from these regions stain positive for the macrophage marker CD68.

Fig. 24A is an ethidium stained agarose gel which contains RT-PCR products amplified using primers for AIF-1 (upper panel) and the reference gene, B-2-microglobulin (lower panel). AIF-1 transcripts were amplified from

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cDNAs derived from the macrophage like cell lines THP-1, U937, and HL-60 (lanes 1-3), but were absent in T cell lines MOLT-4 and Jurket, HepG2 cells, HUVE cells, and HSCM cells (lanes 4-8).

- 5           Fig. 24B is an ethidium stained agarose gel which contains RT-PCR products amplified using primers for AIF-1 (upper panel) and the reference gene, B-2-microglobulin (lower panel). AIF-1 transcripts were amplified to various degrees from cDNAs derived from each of six  
10 endomyocardial biopsies from human cardiac allografts.

#### Detailed Description

##### Lewis to F344 rat cardiac transplantation.

- A rat heterotopic abdominal cardiac transplantation model was used to study transplant  
15 arteriosclerosis and cardiac rejection. (Cramer et al., 1993, *supra*; Adams, D.H., N.L. Tilney, J.J. Collins, and M.J. Karnovsky, 1992, Experimental graft arteriosclerosis. I. The Lewis-to-F344 allograft model, *Transplantation*, 53:1115-1119.) The combination of Lewis  
20 rat donors and F344 rat recipients results in long-term graft survival and a time-dependent development of arteriosclerotic lesions that resemble those in human transplant vessels on histologic examination (Cramer et al., 1993, *supra*; Adams et al., *supra*), and thus is a  
25 suitable animal model for this disease.
- Immunohistochemical studies using antibodies against monocytes, T-cells, and smooth muscle cells have shown that arteriosclerotic lesions develop in 3 distinct stages (Cramer, D.V., G.D. Wu, F.A. Chapman, E. Cajulis,  
30 H.K. Wang, and L. Makowka, 1992, Lymphocytic subsets and histopathologic changes associated with the development of heart transplant arteriosclerosis, *J. Heart Lung Transplant*, 11:458-466; Adams, D.H., L.R. Wyner, and M.J. Karnovsky, 1993, Experimental graft arteriosclerosis. II.

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Immunocytochemical analysis of lesion development, *Transplantation*, 56:794-799). In the first 30 days, the neointimal lesions are composed of infiltrating inflammatory cells (rather than smooth muscle cells), which are predominantly macrophages with fewer lymphocytes. Between 45 and 90 days, the infiltrating inflammatory cell population in the neointima decreases as intimal smooth muscle cells appear. In the last phase (beyond 90 days), the neointima is maximally expanded, often obliterative, and composed predominantly of smooth muscle cells with fewer infiltrating mononuclear cells. The early and persistent presence of monocytes/macrophages in the first stage of arteriosclerosis suggests a prominent role for the macrophage in the initial phase of chronic rejection. To date there are few studies examining specific molecular mechanisms that may regulate the infiltration or function of macrophages in chronically rejecting hearts.

Heterotopic abdominal cardiac transplantation was performed using Lewis donor hearts as described (Adams et al., *supra*) in an allogeneic combination involving F344 recipients. The syngeneic combination, involving Lewis recipients, was performed to assess the contribution of surgical manipulation to the inflammatory response. Lewis hearts that had been harvested but not transplanted were used as reference groups matching the strain of donor or grafted hearts. At the time of harvest, both the host (recipient) and the transplanted hearts were collected for histologic analysis and RNA extraction. The host heart served as a reference that had been exposed to the same circulation but was normal on histologic examination. In some studies, the host spleen was also harvested for a comparison of transcription patterns in an organ rich in inflammatory cells but free of local allogeneic stimulation.

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Transplanted hearts were harvested at 7 and 14 days prior to the development of neointimal thickening. This strategy allowed the detection of transcriptional changes preceding functional changes. At the time of harvest, midventricular sections were taken for histologic analysis and snap frozen in liquid nitrogen for RNA extraction.

RNA isolation and Northern analysis.

Heterotopic abdominal cardiac transplantations were performed and samples were collected as described (Russell, M. E., Adams, D. J., Wyner, L., Halnon, N. J., Yamashita, Y. & Karnovsky, M. J., 1993, *Proc. Natl. Acad. Sci. USA*, 90:6086-6090; Adams, D. H., Tilney, N. L., Collins, J. J. & Karnovsky, M. J., 1992, *Transplantation*, 53:1115-1119, both of which are herein incorporated by reference). For allogeneic transplantations, Lewis rats were used as graft donors and F344 rats were used as recipients. Total cellular RNA was extracted from heart tissue with RNAzol B (Tel-Test, Friendwoods, TX) according to the manufacturer's instructions. Samples of total RNA (20 µg) were fractionated in 1% formaldehyde/agarose gels and transferred onto nylon-supported nitrocellulose (Micron Separation, Boston, MA) by standard capillary blotting techniques. Equivalent loading of samples was verified by ethidium bromide staining of the ribosomal bands. Specific probes were generated by labeling reamplified or cloned cDNA fragments with [ $\alpha^{32}$ P]dCTP by using a random prime DNA labeling kit (Boehringer Mannheim Biochemicals, Chicago, IL). Nucleic acids were cross-linked to the membrane with ultraviolet light (Stratagene, Los Angeles, CA). Hybridization was completed with cDNA probes labeled with  $^{32}$ P dCTP and the blots were washed under high-stringency conditions (0.2 × SSC, 0.1% SDS at 60 °C). Blots were

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exposed to PhosphorImager screens at 25 °C or to Kodak X-Omat AR film with an intensifying screen at -70 °C.

Differential mRNA display

Differential mRNA display analysis was carried out  
5 as described (Liang, P. & Pardee, A. B., 1992, *Science*,  
257:967-971; Liang, P., Averboukh, L. & Pardee, A. B.,  
1993, *Nucl. Acids Res.*, 21:3269-3275, both of which are  
herein incorporated by reference), except that *in vivo*  
rather than *in vitro* samples were used and six rather  
10 than two samples were compared simultaneously, e.g. cDNA  
from 6 separate RNA populations representing 2 syngeneic  
hearts (normal on histologic examination) and 4  
allografted hearts (with early indications of chronic  
cardiac rejection). Control studies included the  
15 substitution of water for cDNA or the omission of reverse  
transcriptase in the cDNA synthesis. The cDNA and PCR  
reactions were modified as follows. Total RNA (0.5 µg)  
was reverse transcribed in a 50-µl reaction using  
Superscript reverse transcriptase (Gibco-BRL Life  
20 Technologies, Baltimore, MD) and the degenerate oligo dT  
primer, T<sub>12</sub>VC or T<sub>12</sub>VA (where V represented a mixture of  
dG, dA or dC) (Genosys, The Woodlands, TX). Control  
reactions were performed in the absence of reverse  
transcriptase. The cDNAs were then amplified by PCR in  
25 the presence of  
[γ-<sup>35</sup>S]dATP on a Perkin Elmer 9600 thermal cycler, and  
control studies were performed in which water was  
substituted for cDNA. The reactions (20 µl) included  
arbitrary 10-mers (Kit A, Operon Technologies, Alameda,  
30 CA) as 5' primers and T<sub>12</sub>VC or T<sub>12</sub>VA as 3' primers. PCR  
parameters for the 40-cycle reaction were as follows:  
denaturation at 94°C for 15 seconds, annealing at 40°C  
for 60 seconds, and extension at 70°C for 20 seconds.  
Radiolabeled PCR amplification products were analyzed  
35 using electrophoresis. Variability of 5-20% in the

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- number and intensity of bands among given samples on repeated PCR analyses, as well as among different allogeneic or syngeneic samples in the same PCR analysis was observed. To confirm the reproducibility of
- 5 amplification for selected bands, the reactions were repeated at least three times with different preparations of cDNA. Differentially upregulated bands were defined as those that were consistently present in all four allogeneic samples and absent in both syngeneic samples.
- 10 Differentially downregulated bands were defined as those present only in syngeneic samples. PCR product bands were recovered from sequencing gels using electroelution and reamplified in a 40-cycle PCR reaction (80  $\mu$ l) in the absence of isotope. Reamplified cDNAs ranging from 100
- 15 to 500 bp were used for cloning into plasmid vectors and as templates for random priming.

#### Cloning

- Reamplified PCR products were directly cloned into the TA cloning vector PCR II (Invitrogen, San Diego, CA).
- 20 The inserts were used as probes in Northern blot analysis of RNA from various cardiac allografts, syngrafts, and host hearts to confirm the allograft-specific hybridization pattern. The partial 3' cDNA fragment was then used to screen ~500,000 plaques from a bacteriophage
- 25 lambda, custom Uni-ZAP cDNA library prepared from 14-day cardiac allograft poly(A)+ RNA (Stratagene). Positive clones were isolated and rescued as plasmids, and their identity was verified by demonstration of allograft-specific hybridization on Northern blot analysis. DNA
- 30 sequencing of both sense and anti-sense strands was performed with the Sequenase 2.0 kit (United States Biochemical, Cleveland, OH) on double-stranded plasmid DNA clones and subclones. Nucleotide and predicted amino acid-sequence searches of the GenBank and EMBL data bases

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were performed with the (FASTA program GCG software package).

Inflammatory cell populations

Isolated splenocytes were obtained by sieving  
5 splenic tissue into DMEM medium (Gibco-BRL Life Technologies, Baltimore, MD) using methods well known in the art. These cells were fractionated with Ficoll-Paque (Pharmacia, Piscataway, NJ), and the mononuclear fraction was cultured at a density of  $2-4 \times 10^6$  cells/ml in a  
10 humidified incubator at 37°C with 5% CO<sub>2</sub>. A lymphocyte-enriched cell population was obtained by nylon wool purification, where nonadherent cells are removed by gentle washing. Cells adhering to plastic dishes were stained with an anti-macrophage antibody, ED1  
15 (Bioproducts, Inc., Indianapolis, IN), with greater than 70% positive indicating an enrichment for phagocytic cells. In contrast, few of the nonadherent cells were ED1 positive.

Where indicated, lipopolysaccharide (1 ng/ml,  
20 Sigma, St. Louis, MO), rat interferon- $\gamma$ , (100 U/ml, Gibco-BRL Life Technologies, Baltimore, MD), concanavalin A (2  $\mu$ g/ml, Sigma, St. Louis, MO) or buffer alone was added to isolated cell populations. The cells were harvested 3 hours later. Peritoneal inflammatory rat  
25 macrophages were elicited with thioglycolate medium using standard methods (Steinbeck, M.J., A.U. Khan, and M.J. Karnovsky, 1993, Extracellular production of singlet oxygen by stimulated macrophages quantified using 9,10-diphenylanthracene and perylene in a polystyrene film, J.  
30 *Biol. Chem.*, 268:15649-15654). Peritoneal exudate cells were collected 4 days after induction of inflammation, separated on a Ficoll-Paque gradient, and plated at a density of  $2 \times 10^6$  cells/ml. At least 90% of the adherent cell population were judged to be macrophages by  
35 morphologic criteria and antibody staining. Total RNA



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was extracted from these isolated cells, the quality of which was assured by evaluation of ribosomal RNA after 1  $\mu$ g had been separated on 3 mm agarose gels prior to cDNA preparation.

5 Semiquantitative reverse-transcription PCR assay

As an alternative to Northern blot analysis, a semiquantitative, reverse-transcription PCR analysis to compare Gal/GalNAc macrophage lectin transcript levels was performed to allow conservation of RNA when samples were limited. A reverse-transcription PCR technique developed to measure differences in monocyte chemoattractant protein-1 transcript levels (Russell et al., 1993 *supra*) was modified for use with Gal/GalNAc macrophage lectin. cDNA synthesis was completed with random primers (2.5  $\mu$ g total RNA per reaction). Oligonucleotides were synthesized by Genosys, The Woodlands, TX. The sequences were CCT AGA AAC CCT GAG AAC (SEQ ID NO: 31) for the 5' primer and GAG TGC CGC TTA TTG TAG (SEQ ID NO: 32) for the 3' primer, chosen from the sequence analysis of our cDNA clone to result in a 941-bp product. The thermal cycling parameters were denaturation at 94°C for 15 seconds, annealing 54°C for 20 seconds, and extension for 60 seconds (with a final extension of 7 minutes at the end of all cycles). For quantitative PCR analyses, 150,000 cpm of  $^{32}$ P-dCTP was included in the PCR reaction. The products were separated on 1% agarose gels which were dried and exposed to PhosphorImaging screens for 12 hours. The amount of incorporated  $^{32}$ P in amplified product bands was then measured by volume integration (Imagequant Software, Molecular Dynamics, San Francisco, CA).

To identify the optimum PCR conditions for accurate measurement of gene transcript levels, the linear assay range with respect to cycle number and starting template concentration was established by using

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different dilutions of cDNA. The measurement of Gal/GalNac macrophage lectin transcript levels was then completed within these ranges (30 cycles, with starting cDNA dilutions of 1.25  $\mu$ l). PCR amplification with

5 G3PDH, a ubiquitously expressed gene, was used as a control to assess variations in total RNA or cDNA loading between samples. Corrected Gal/GalNac macrophage lectin values were derived by dividing the measured amplified product value by the mean of the G3PDH value obtained for

10 that cDNA from at least 3 analyses. PCR analyses were completed on each set of cDNAs at least four times. Results were subjected to multiple analysis of variance (MANOVA) without replication. If a difference was significant, individual comparisons were made by the

15 student's t test, corrected by the Bonferroni method. Although there were variations in absolute values derived from different experiments, relative differences between cDNA sets analyzed at the same time were preserved.

Comparison of corrected Gal/GalNac macrophage lectin

20 levels Differences in corrected Gal/GalNac macrophage lectin transcript levels were examined in 3 separate studies. The first study was completed to compare differences in transcript levels at various time points after cardiac transplantation. The 10 cDNAs in

25 this time-course study included samples from 4 cardiac allografts harvested 7, 14, 28, and 75 days after transplantation compared with 1 day-0 Lewis heart, a total of 3 paired host hearts from days 7, 14, and 28, and a day-14 Lewis syngraft with its paired host heart.

~~30 The second cDNA analysis examined whether Gal/GalNac~~

macrophage lectin induction occurred systemically or locally. cDNA levels in the host spleen (principal source of inflammatory cells) were compared with those in the allografted heart. The 6 cDNAs analyzed were derived

35 from 2 allogeneic cardiac transplants: 1 harvested at 7

- 25 -

days, the other at 28 days. At each time point, the cDNAs from the host heart, allografted heart, and the host spleen were compared. In the third cDNA study, Gal/GalNAC macrophage lectin gene expression in various  
5 populations of isolated rat inflammatory cells was examined. Of the 9 cDNAs studied, 6 were prepared from splenocytes (both adherent and nonadherent, each type stimulated with buffer, concanavalin A, and lipopolysaccharide/ interferon- $\gamma$ ), 2 from separate  
10 thioglycolate-elicited macrophage preparations, and 1 from a 14-day cardiac allograft.

#### In situ hybridization

*In situ* hybridization was completed as described (Arceci, R.J., A.A.J. King, M.C. Simon, S.H. Orkin, and  
15 D.B. Wilson, 1993, Mouse GATA-4: a retinoic acid-inducible GATA-binding transcription factor expressed in endodermally derived tissues and heart, *Mol. Cell. Biol.*, 13:2235-2246, herein incorporated by reference), using 5-micron frozen sections obtained from 7-day cardiac  
20 allografts and paired host hearts. To generate radiolabeled antisense and sense transcripts, the full-length 1.4-kb Bluescript cDNA was linearized and transcribed with T7 or T3 polymerase using  $^{35}$ S-UTP. The  
specificity of the antisense riboprobe was confirmed by  
25 hybridization in Northern analysis to 1.4-kb transcripts in lanes with cardiac allograft total RNA, but not in lanes with day-0 heart total RNA.

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EXAMPLE 1: Methods of screening for differentially expressed genes involved in allograft rejection

For most genes, expression is regulated at the level of transcription. Conventional measurements of mRNA transcript levels are usually confined to selected genes of interest and often require information about the gene sequence. In contrast, PCR-based differential display techniques circumvent this constraint by allowing comparison of gene expression patterns between two cell populations (Liang et al., 1992, supra) or between various murine organs (Welsh, J., Chada, K., Dalal, S. S., Cheng, R., Ralph, D. & McClelland, M., 1992, Nucl. Acids Res., 20:4965-4970). One of the principal advantages of differential display is that it permits the simultaneous identification of genes that are up- as well as downregulated. Thus differential display has the potential to identify a spectrum of molecular factors (known and unknown) that are differentially regulated in cells under various conditions.

Studies of allograft rejection in humans have been restricted by the limited availability of tissue for analysis. Clinical specimens are heterogenous in their degree of chronic rejection, their extent of superimposed disease processes, and the period between the time they are obtained and the time of transplantation. Also, transplanted hearts obtained at autopsy are not suitable for analysis (which requires viable tissue), and the utility of endomyocardial biopsy specimens is limited by their small size. Moreover, the restricted extent of arteriosclerotic lesions that follow transplantation suggests that the process is locally regulated; thus, studies measuring systemic levels of factors implicated in chronic rejection may not accurately reflect levels within the graft (Fyfe, A., Daly, P., Galligan, L., Pirc, L., Feindel, C. & Cardella, C., 1993, J. Am. Coll. Cardiol, 21:171-176).

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Differential mRNA display

To identify transcriptionally regulated genes potentially involved in chronic rejection, differential mRNA display patterns for hearts from syngeneic

5 transplantations were compared with those for hearts from allogeneic transplantations. Syngeneic hearts were normal on histologic examination, whereas 7- and 14-day allogeneic hearts showed luminal monocyte adhesion and infiltration without intimal thickening. PCR

10 amplifications were performed with 27 primer combinations on all six samples and identified twelve PCR products, designated Bands 1-12. These bands were differentially expressed between allogeneic and syngeneic tissue. Figs. 9A-9C show PCR amplifications obtained with three

15 separate primer combinations. Four representative PCR products (Bands 1, 2, 11, and 12) were identified. These bands were reproducibly present in the allogeneic samples (Lanes 3-6), but not in the syngeneic samples (Lanes 1 and 2), in each of the three analyses identified (see

20 Figs. 9A-9C).

RNA blot analysis with PCR-amplified fragments

To confirm the gene regulation patterns observed in the differential display study, the twelve bands described above were recovered, reamplified, and used to

25 probe RNA blots prepared with RNAs from syn- and allogeneic transplantations. When used as probes, four of the twelve PCR-amplified fragments (Bands 1, 2, 11, and 12) generated hybridization patterns that reproduced the allograft-specific increase in expression (Fig. 10A,

30 Lanes 3-6). All four of these probes generated two hybridization signals of different sizes. The two signals identified by the Band-1 and -11 probes were both specifically present in allografted tissues (Lanes 3-6, arrows) and absent in syngrafted tissues (Lanes 1 and 2).

35 In contrast, the Band-2 and -12 probes each generated one

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allograft-specific signal (arrows) reproducing the differential display pattern, as well as a second signal present in all six lanes (arrowheads) that did not reproduce the differential display pattern. Three reamplified PCR fragments hybridized nonspecifically to all six lanes. Five of the twelve cDNA probes did not detect any transcripts (data not shown). Such transcripts may not have been detected because their levels were below the sensitivity of the RNA blot analysis. As a control, RNA loading in all six lanes was confirmed by hybridization with the ribosomal reference gene 36B4 (Laborda et al., supra).

#### RNA Blot Analysis with Cloned Fragments

The PCR products that generated one or more allograft-specific hybridization patterns were then cloned and used as hybridization probes in RNA blot analysis to identify single clones corresponding to specific mRNA transcripts (Fig. 10B and Table 1). For Bands 2 and 12, individual cDNA clones were identified that produced hybridizations in an allograft-specific fashion. Identification of individual clones was more arduous for the bands that had generated two allograft-specific signals in the initial RNA blot analysis.

Two separate mechanisms account for the transcripts of two sizes observed for Band 1 compared with Band 11. For Band 1, an individual cDNA clone generated two faint hybridization signals of 3.5 kb and 1.5 kb specifically in the allograft samples (Lanes 3-6). This suggests that the two mRNAs were generated by alternative splicing of a common mRNA precursor, by a gene duplication event, or, less likely, by a common regulatory pattern for genes that share some homology. For Band 11, however, two independent cDNA clones with allograft-specific regulation were isolated: one hybridizing to a 1.0-kb transcript and the other to a

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3.5-kb transcript. These two distinct clones hybridizing to transcripts of two sizes demonstrate that PCR-amplified products from a display band can contain a number of distinct cDNA fragments derived from different genes (Table 1). Thus, in the initial RNA blot screen, the PCR reamplified fragment (which may contain a mixture of PCR products) is more likely to identify differentially regulated transcripts than are individual cDNA clones.

10 Sequence homology

Cloned cDNA fragments that generated allograft-specific hybridization patterns in the RNA blot analysis were sequenced, and preliminary homology searches were performed. The results are summarized in Table 1. The cDNA fragment from Band 2 was found to be highly homologous to rat Gal/GalNAc lectin macrophage. The 382-bp fragment was 98% identical to bases 975-1357 of the published lectin sequence (Ii, M., Kurata, H., Itoh, N., Yamashina, I. & Kawasaki, T., 1990, J. Biol. Chem., 265:11295-11298). This region includes 114 bp of open reading frame as well as 3' untranslated sequences. Homologies with two distinct genes were identified for the two independent clones associated with Band 11. The cDNA fragment (110 bp) that hybridized to the smaller mRNA transcript (1.0 kb) was 79% homologous to the 3' untranslated region of a partial cDNA sequence obtained from a mouse ubiquitin-like gene (Kumar, S., Tomooka, Y. & Noda, M., 1992, Biochem. Biophys. Res. Commun., 185:1155-1161). The cloned fragment (119 bp) that hybridized to the larger transcript (3.5 kb) was 92% homologous to a partial cDNA sequence of the mouse nuclear P1 gene (Hershko, A. & Ciechanover, A., 1992, Annu. Rev. Biochem., 61:761-807). The homologous region of the P1 gene was located within the open reading frame (bases 1-120) and not at the 3' end. Therefore, in this

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instance, the 3' primer of the initial PCR reaction hybridized to an internal sequence. To date no significant homology with any published gene for the sequences obtained from the Band-1 and -12 cDNA fragments has been found, suggesting that they represent previously unknown genes associated with chronic cardiac rejection.

Each differential display analysis was performed at least three times to reduce nonspecific (background) PCR signal interference, and the selection of cDNA bands chosen for further study was restricted to those that reproduced the regulation pattern of the first RNA blot analysis in at least three analyses.

Using 27 primer combinations, twelve differential display cDNA bands that were reproducibly up- or downregulated in allogeneic hearts were identified. For four of the twelve bands, this allograft-specific regulation was reproduced on RNA blot analysis. Two unknown genes and three known genes not previously implicated in chronic rejection were identified.

The screening methods of the invention are designed to identify mediators that might be selective for or specific to chronic rejection. Three known genes never before associated with transplant rejection and two novel genes have been identified using the methods of the invention. The three upregulated genes with identifiable homologies correspond to the Gal/GalNAC macrophage lectin, the nuclear P1 gene, and a ubiquitin-like gene.

The link between the macrophage lectin gene and chronic rejection is important because, prior to the invention, the factors responsible for macrophage accumulation in the early phase of the process were not known. Lectins are cell-surface molecules that mediate cell-cell interactions by recognizing specific sugar molecules on adjacent cells (Sharon et al., supra). The murine Gal/GalNAC-specific lectin was originally



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identified by immunofluorescence on thioglycolate-elicited and OK-432 (a streptococcal antitumor preparation)-activated macrophages but not on unstimulated or resident macrophages (Oda et al., 1989, supra), suggesting that this lectin may be a marker of macrophage activation.

The mouse P1 protein, a homologue of yeast MCM3 (minichromosome mutant), plays a role in the initiation of DNA replication in association with DNA polymerase primase (Thoemmes, P., Fett, R., Schray, B., Burkhart, R., Barnes, M., Kennedy, C., Brown, N. C. & Knippers, R., 1992, Nucl. Acids Res., 20:1069-1074). The identification of elevated transcript levels for the P1 gene in cardiac allografts compared with syngrafts suggests the presence of replicating cells at early points in chronic rejection. Localizing the specific cell type that expresses P1 gene transcripts (or protein) by *in situ* hybridization or immunohistochemistry may help elucidate early proliferative processes in chronic rejection.

The third known gene upregulated in cardiac allografts is homologous to the 3' region of a murine ubiquitin sequence (Kumar et al., supra). As its name implies, ubiquitin is expressed in all eukaryotic cells. However, ubiquitin gene transcripts appear to be upregulated specifically in allogeneic tissue. Although ubiquitin is involved in a wide variety of regulatory functions within the cell, its role in protein degradation is best understood. In that process ubiquitin is covalently attached to a specific protein target which is then recognized and degraded (Hershko et al., supra). The conjugation of ubiquitin to a protein is essential to normal protein turnover. However, the induction of ubiquitin is also part of the cellular response to stress, damage, or injury (Mayer, R. J.,

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Arnold, J., Laszlo, L., Landon, M. & Lowe, J., 1991, Biochim. Biophys. Acta, 1089:141-151). Although ubiquitin's specific role in chronic cardiac rejection is not clear, it is possible that ubiquitin is involved in the response to immune injury thought to initiate allograft arteriosclerosis.

#### Advantages

The screening methods of the invention can be used to identify mediators associated with chronic allograft rejection, a complex, multicellular disease process using differential display technology to detect upregulated or downregulated allograft gene transcripts. Differential display technology has been used to study breast cancer (Liang et al., 1992, supra; Liang et al., 1993, supra; Liang, P., Averboukh, L., Keyomarsi, K., Sager, R. & Pardee, A. B., 1992, Cancer Res., 52:6966-6968; Sager, R., Anisowicz, A., Neveu, M., Liang, P. & Sotiropoulou, G., 1993, FASEB J., 7:964-970). However, in contrast to the breast-cancer studies, which compared two populations of *in vitro* cell lines at once, the screening methods of the invention compare whole tissue from allogeneic transplantations (where chronic rejection develops) with whole tissue from syngeneic transplantations (where rejection is absent). One important advantage of this approach is that the pathophysiologic environment associated with the chronic disease process is preserved. The invention provides a method of analyzing a mixture of both resident and infiltrating cells, as well as the complex network of regulatory stimuli that may have been impossible to reproduce in isolated cells *in vitro* (Liaw, L. & Schwartz, S. M., 1993, Arterioscler. Thromb., 13:985-993). Also, because the screening method can compare a number of tissue samples at once, e.g., a series of six transplanted hearts simultaneously, the identification of factors that might be related to a

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single animal or procedure rather than to the disease itself can be avoided.

With the identification of these five candidate mediators of chronic rejection, utility of the screening methods of the invention, e.g., those which utilize differential mRNA display analysis, to identify molecular factors associated with complex multicellular processes, has been demonstrated. For identification of allograft-specific factors, an increase or decrease in allograft gene transcript of at least 4 times the amount of corresponding syngraft gene transcript is preferable.

In the case of chronic rejection, which affects the donor organ only and spares host organs, differential mRNA display can be used to examine the transplanted heart as well as its infiltrating cell populations. Given that inflammatory cells are often activated in a manner specific to their microenvironment, the power of this technique resides in its preservation of infiltrating cells and the complex network of regulatory influences in the tissue under investigation. *In vitro* systems investigating single cell types cannot reproduce the spectrum of interactions present in diseased tissue *in vivo* because they lack the counterregulatory effects of neighboring cells. The differentially regulated factors identified in this manner are therefore more likely to be of direct clinical relevance. Finally, the methods of the invention allow the identification of candidate factors that may be beyond the scope of established theories of chronic rejection.

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30 EXAMPLE 2: Assays to diagnose rejection of an allograft

As described above, several genes (Gal/GalNAc-macrophage lectin, AIF-1, AIF-2, ubiquitin and P1) which are differentially expressed in the allograft have been identified using the screening methods of the invention.

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Other genes can be identified using the same methods. Having identified genes which are differentially expressed in an allograft compared to a syngraft, detection of expression of these genes either at the  
5 level of transcription, e.g., by PCR, Northern blot, differential mRNA display, or *in situ* hybridization, or at the level of translation/protein production, e.g., by FACS, Western blot, or *in situ* immunostaining, provides a valuable tool for early and reliable diagnosis of  
10 transplant rejection. For example, Gal/GalNAc macrophage lectin transcript or protein levels in transplanted heart samples obtained by endomyocardial biopsy could serve as clinical markers of macrophage infiltration. These levels might provide prognostic information about the  
15 degree of chronic rejection or the rate at which arteriosclerosis is progressing.

One of the major advantages of such a diagnostic approach is that the screening methods of the invention allow early detection of events which lead to allograft  
20 rejection, and thus facilitate early intervention to prevent or inhibit rejection of the transplanted organ. Another advantage is that the diagnostic methods of the invention can be performed on a very small amount of tissue which may be obtained using standard biopsy  
25 techniques known in the art.

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EXAMPLE 3: Therapeutic applications for differentially expressed allograft genes

As described above, an increase in the amount of an allograft gene transcript compared to the corresponding syngraft gene transcript indicates that the allograft transcript encodes a mediator of allograft rejection. Thus, allograft rejection in patients may be decreased or inhibited using gene therapy in which a portion of the antisense strand of the upregulated gene is introduced into the cells in which the gene is transcribed. The antisense oligonucleotide (either RNA or DNA) may be directly introduced into the cells in a form that is capable of binding to the transcripts. Alternatively, a vector containing sequence which, once within the target cells, is transcribed into the appropriate antisense mRNA, may be the species administered to the patient's cells. An antisense nucleic acid which hybridizes to the mRNA of the target gene can decrease or inhibit production of the polypeptide product encoded by the gene, by forming a double-stranded segment on the normally single-stranded mRNA transcript, and thereby interfering with translation.

~~A DNA which is expressed as a transcript antisense~~ to a portion of the target gene may be operably linked to appropriate expression control sequences and introduced into target cells of the patient by standard vectors and/or gene delivery systems. Suitable gene delivery systems may include liposomes, receptor-mediated delivery systems, naked DNA, and viral vectors such as herpes viruses, retroviruses, and adenoviruses, among others.

A therapeutic composition is provided which includes a pharmaceutically acceptable carrier and a therapeutically effective amount of a nucleic acid which is capable of inhibiting translation of the target mRNA, either directly or by being transcribed into an antisense

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transcript which inhibits translation. The therapeutic composition may also include a gene delivery system as described above. Pharmaceutically acceptable carriers are biologically compatible vehicles which are suitable  
5 for administration to an animal: e.g., physiological saline. A therapeutically effective amount is an amount of the DNA of the invention which is capable of producing a medically desirable result in a treated animal, e.g.,  
10 downregulation of the differentially expressed allograft gene.

As an alternative to the antisense-based therapy described above, one could employ polyclonal or monoclonal antibodies specific for the polypeptide product of the overexpressed allograft polypeptide, in  
15 order to block that polypeptide's activity in vivo. Similarly, one could employ polypeptide inhibitors to block activity of the differentially expressed allograft polypeptide, e.g., fragments of the polypeptide which block binding of the polypeptide to its ligand. The  
20 antibody or other polypeptide-based therapeutic can be delivered by standard means, such as intravenous injection.

As is well known in the medical arts, dosages for any one patient depends upon many factors, including the  
25 patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently. Dosages for the compounds of the invention will vary, but a preferred dosage for  
30 ~~intravenous administration is from approximately  $10^6$  to~~  
 $10^{22}$  copies of the nucleic acid molecule.

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EXAMPLE 4: Rat AIF-1

As described above, the differential display screening methods of the invention were used to identify two novel genes which are upregulated in rat cardiac allografts with transplant arteriosclerosis. Bands 1 and 12 (see Figs. 9A-9C) were harvested, reamplified, and used as probes in Northern analysis. The allograft-specific induction pattern was confirmed in the RNA extracted from the original 6 samples, identifying gene transcripts of 0.7 kb. Following Northern blot confirmation, partial cloning, sequence analysis of AIF-1 (331 bp sequenced/400 bp fragment) (SEQ ID NO:1), and a homology search were completed. Partial cloning, sequence analysis, and a homology search were also completed for AIF-2 (359 bp/-450 bp sequenced) (SEQ ID NO:2, 3). A database search using these fragments revealed no alignment with known sequences.

Cloning and characterization of full-length AIF-1 cDNA

A custom-made rat cardiac allograft cDNA library was obtained from Stratagene, Inc. To isolate the full-length cDNAs, the 14-day old cardiac allograft cDNA library was screened with the partial cDNA fragments identified in the differential display. Fifteen AIF-positive phagemid clones were obtained; however, eight were identical in sequence. The full-length cDNA of AIF-1 (SEQ ID NO:4) is 627 bp long and contains a 70-bp 5' untranslated region, a continuous open reading frame of 441 bp, and a 116-bp 3' untranslated region that includes one potential polyadenylation sequence.

Translation of the open-reading frame predicts a polypeptide of 147 amino acids, with a calculated molecular mass of 16.8 kD. Charged amino acids comprise 35% of the predicted polypeptide. The profile generated by the Kyte-Doolittle algorithm (Fig. 11) predicts a hydrophilic polypeptide without significant hydrophobic

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stretches, which are usually associated with membrane-spanning proteins.

Database searches revealed homology with genomic sequences obtained from a 90-kb segment of the human HLA class III region (which had been systematically sequenced in a mapping effort) (Iris et al., Nature Genet. 3:137-145, 1993). Homology ranged from 68-93% over the entire AIF-1 cDNA sequence. Alignment was identified in a segment 7 kb upstream of the BAT-2 gene. To date, no coding sequences have been submitted to the GenBank and EMBL data bases in this region; thus, AIF-1 appears to represent a novel cDNA. Motif analysis of the predicted amino acid sequence identified a potential EF-hand domain that is characteristic of an evolutionary family of calcium-binding proteins (Strynadka et al., Ann. Rev. Biochem. 58:951-998, 1989). Typically, the conserved amino acids within the loop are involved in binding of the calcium ion. AIF-1 matches the consensus sequence of the EF-hand loop supplied through the Prosite data base (release 9.2), with the exception of position 12. This conserved position-12 residue (usually glutamic acid or aspartic acid) is replaced by a serine residue in the AIF-1 sequence. In addition to the conserved loop sequence, AIF-1 has some alignment within the entire EF-hand region to other members of the family, such as mouse troponin C (51% similar or identical amino acids) (Pamacek et al., J. Biol. Chem. 265:15970-15976, 1990) and human calmodulin (48% similar or identical amino acids) (Koller et al., Biochim. Biophys. Acta. 1163:1-9, 1993).

#### Northern and genomic Southern analysis.

Total RNA was isolated with RNazol B (Tel-Test, Inc., Friendswood, TX). Northern blots were prepared with 20 µg of total RNA as described above. Genomic DNA was isolated and digested with the indicated restriction



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endonucleases, electrophoresed through 0.8% agarose gels, and transferred to nitrocellulose (Micron Separations, Westboro, MA) by capillary transfer as described (Russell et al., Blood 72:1833-1836, 1988). Hybridization with  
5 cDNA probes labeled with  $^{32}\text{P}$  dCTP by random priming (Boehringer-Mannheim, Indianapolis, IN), and high-stringency washes ( $0.2 \times \text{SSC}$ , 0.1% SDS at  $60^\circ\text{C}$ ), were performed as described above. The AIF-1 cDNA hybridized to genomic DNA from rats, mice, and humans (Fig. 12),  
10 demonstrating evolutionary conservation across these species. The presence of only one or two bands under high-stringency conditions suggests that AIF-1 is encoded by a single-copy gene.

Semiquantitative reverse-transcriptase PCR assay.

15 The reverse-transcriptase PCR technique described above was used to measure AIF-1 transcript levels. cDNA synthesis was completed with random primers ( $2.5 \mu\text{g}$  of total RNA per reaction). Oligonucleotides were synthesized by Genosys Biotechnologies (The Woodlands,  
20 TX). To amplify rat cDNAs, the following primers were used:  
5' primer GTCAATTCGCTATGAGCCAGAGCAAG (SEQ ID NO: 33) and  
3' primer GAAGAAGCAGTTGTGAGCGTCGACCAA, (SEQ ID NO: 34), a  
~~combination that resulted in a 543-bp product.~~ For  
25 murine and human cDNAs, an internal set of primers were used:  
5' ATCCCAAGTACAGCAGTGATGAGG (SEQ ID NO: 35) and  
3' GTCCCCCAGCCAAGAAAGCTATTT (SEQ ID NO: 36), which  
generated a 329-bp PCR product. Reaction conditions were  
30 as described above. The thermal cycling parameters were  
denaturation at  $94^\circ\text{C}$  for 15 sec, annealing at  $56^\circ\text{C}$  for 20 sec, and extension for 60 sec (with a final extension of 7 min at the end of all cycles). For quantitative PCR analyses, 150,000 cpm of  $^{32}\text{P}$ -dCTP were included in the PCR  
35 reaction. The products were separated on 1% agarose gels

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which were dried and exposed to PhosphorImaging screens for 24 h, and the amount of  $^{32}\text{P}$  incorporated in the amplified product bands was measured by volume integration (Imagequant software, Molecular Dynamics, Sunnyvale, CA).

To identify the optimal PCR conditions for accurate measurement of gene transcript levels, linear assay ranges were established with respect to cycle number and starting template concentration for various dilutions of cDNA. Measurement of AIF-1 transcript levels was then completed within these ranges (23 cycles and cDNA dilutions of 1.25  $\mu\text{l}$  for both primer combinations). PCR analyses were completed on each set of cDNAs at least 3 times. PCR amplification with G3PDH, a ubiquitously expressed gene, was used as a control to assess variations in total RNA or cDNA loading between samples. Corrected AIF-1 values were derived by dividing the measured amplified product value by the mean of the G3PDH value obtained for that cDNA from at least 3 analyses. Results were subjected to multivariate analysis of variance without replication. If a difference was significant, individual comparisons were corrected by the Bonferroni method. Although there were variations in absolute values derived from different experiments, relative differences between cDNA sets analyzed at the same time were preserved.

In situ hybridization.

In situ hybridization was completed as described above, using 5-micron frozen sections obtained from 28-day cardiac allografts and paired host hearts and spleens. To generate radiolabeled antisense and sense transcripts, the full-length AIF-1 cDNA was linearized and transcribed with T7 or T3 polymerase in the presence of  $^{35}\text{S}$ -UTP. The specificity of the riboprobes was confirmed by hybridization of the antisense probe in

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Northern analysis to 0.7-kb transcripts in lanes with cardiac allograft total RNA but not in lanes with day-0 heart total RNA, and by no hybridization with the sense probe.

5 Protein expression studies.

Recombinant AIF-1 was generated as a fusion protein using the pMAL-c2 (New England Biolabs, Beverly, MA) or the pFLAG-1 (International Biotechnologies Incorporated, New Haven, CT) expression vector according to the manufacturers' instructions. The purified protein was used as an immunogen to generate a polyclonal rabbit antiserum (East Acres Biologicals, Southbridge, MA). Tissue or cellular extracts were prepared by homogenization in 50 mM Tris (pH 8.0), 500 mM NaCl, 20% glycerol, 1 mM dithiothreitol, and 0.5 mM phenylmethanesulfonyl fluoride. Protein extracts (25 µg) were separated on 15% SDS polyacrylamide gels and transferred to polyvinylidene difluoride membranes (Millipore, Bedford, MA). Immunostaining was performed with an enhanced chemoluminescence detection kit (ECL, Amersham, Cleveland, OH) according to the manufacturer's directions, at primary antiserum dilutions of 1:3000. Negative controls included omission of the primary antibody or use of preimmune serum. Immunohistochemical staining of frozen sections from 28-day cardiac allografts, host hearts, and spleens was completed at an antiserum dilution of 1:500 (1 h, 25°C) as described (Russell et al., J. Clin. Invest. 94:722-730, 1994). Negative controls included omission of the primary antiserum, use of preimmune serum, and use of an irrelevant primary antiserum.

In vitro and in vivo regulation of AIF-1 transcript levels.

In vitro stimulation studies of various macrophage cells or cell lines were completed using rat IFN-γ

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(100 units/ml) (Gibco-BRL, Gaithersburg, MD), phorbol 12-myristate-13-acetate (50 ng/ml) (Sigma), or lipopolysaccharide (*E. coli* serotype 0111:B4) (100 ng/ml) (Sigma, St. Louis, MO). To study whether strategies which impair T-cell activation in vivo would alter AIF-1 transcript levels, cDNA samples from two series of transplants performed previously were evaluated. In the first series, the cDNAs were prepared from transplanted and host hearts harvested at day 7 and 28 from recipients fed an anti-inflammatory, essential fatty acid-deficient (EFAD) diet or a control diet. In the second transplant series, the recombinant fusion protein CTLA-4 Ig (Bristol-Myers Squibb, Seattle, WA), which blocks the CD28/B7 costimulatory pathway, was used to inhibit T-cell activation in chronic cardiac rejection (Sayegh et al., J. Am. Soc. Nephrol. 5:989, 1994). These cDNA samples were prepared from 75-day cardiac allografts treated with (a) a single dose of CTLA-4 Ig (0.5 mg intraperitoneally) (n=3), (b) a single dose of CTLA-4 Ig and an intravenous injection of donor splenocyte cells (n=3), or (c) a single dose of cyclosporine\_A (5 mg/kg intramuscularly) (Sandoz, Basel) (n=3). These samples were compared with samples from day-75 syngrafts (n=3) and an untreated (reference) day-75 cardiac allograft (n=1).

25 Northern blot analysis of rat organs.

Northern blot analysis (Fig. 13) showed strong hybridization of the AIF-1 cDNA to 0.7-kb transcripts in total RNA from a day-28 cardiac allograft, spleen, and testis. The increase in AIF-1 transcripts in this cardiac allograft compared with a control heart (day 0), which had been harvested but not transplanted, confirms the allograft-specific pattern identified above. The presence of AIF-1 transcripts in the spleen (a major source of inflammatory cells) as well as the cardiac allograft—the vessels of which are characterized at day

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28 by mononuclear cell infiltration and early intimal thickening--suggests that AIF-1 represents an inflammatory cell transcript.

AIF-1 gene expression increases in cardiac allografts over time.

To study AIF-1 gene expression patterns after cardiac transplantation, transcript levels were measured with a reverse-transcriptase PCR assay in cDNAs derived from cardiac allografts and paired host hearts harvested at various stages of chronic rejection. As seen in the representative analysis that included two transplants from each time point (Fig. 14), AIF-1 transcript levels were significantly higher in cardiac allografts (days 7, 28, 75), in comparison with paired host hearts which had been exposed to the same circulation but had no histologic abnormalities ( $p < 0.003$ ). Transcript levels were also significantly higher in day-75 cardiac allografts ( $n=2$ ) compared with day-75 cardiac syngrafts ( $n=2$ ) ( $p < 0.0001$ ). AIF-1 transcript expression peaked at day 28, with cardiac allograft levels significantly higher in comparison with those at both days 7 and 75 ( $p < 0.001$ ) in 2 separate experimental sets. These findings confirm the allograft-specific and time-dependent expression of AIF-1 transcripts originally observed in Northern blot studies in which the AIF-1 3' cDNA fragment was used as probe.

In situ localization of AIF-1 mRNA to inflammatory infiltrates within cardiac allografts.

In Fig. 15A, silver grains indicating hybridization of the AIF-1 antisense riboprobe cluster over regions of inflammatory cell infiltrates in cardiac allograft sections, and they do not cluster over myocytes. Positive hybridization was seen predominately in the interstitium and perivascular spaces. In splenic tissue, silver grains associated with AIF-1 mRNA were

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identified primarily in regions within the red pulp (not shown). There was no significant hybridization to host hearts (not shown) or when the sense probe was used (Fig. 15B).

5 AIF-1 transcript levels in inflammatory cell populations.

To further characterize the cell type(s) that express AIF-1 transcripts, a series of isolated rat cell populations were analyzed by Northern blotting (Fig. 16). AIF-1 transcripts were expressed by bone marrow-derived  
10 macrophages, BCG-elicited peritoneal macrophages, and casein-elicited peritoneal neutrophils but not significantly by nylon wool-purified lymphocytes, aortic smooth muscle cells, or bone marrow stem cells. In other studies, AIF-1 transcripts were detected in  
15 thioglycolate-elicited peritoneal macrophages and adherent splenocytes. By the reverse-transcriptase PCR assay, AIF-1 transcripts were also present at low levels in a variety of unstimulated murine and human myeloid cell lines, including J744A.1, RAW264.7, P388D.1, HL60,  
20 U937, and THP-1. Transcripts were not detected in lymphocytic leukemia cell lines (Jurkat or MOLT-4). Thus, AIF-1 appears to be expressed predominately by cells of the myeloid lineage (monocytes/macrophages and neutrophils).

25 Immunoblotting with anti-AIF-1 serum.

A single band of approximately 17 kD was detected with polyclonal rabbit anti-AIF-1 serum in extracts from cardiac allografts, splenic tissue, and bone marrow-derived macrophages propagated in vitro (Fig. 17). The  
30 absence of staining in host hearts, lymphocytes, and bone marrow cells reproduced the patterns shown for gene transcripts.

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Immunohistochemical localization of AIF-1 antigen in cardiac allografts.

Immunostaining identified a subset of positively labeled mononuclear cells within cardiac allografts (Fig. 18A). The positive cells showed a cytoplasmic staining pattern and were found in regions of perivascular and interstitial infiltration. Besides these inflammatory mononuclear cells, none of the parenchymal cell types within the cardiac allograft stained positive. In splenic tissue, scattered positive cells were identified predominately in the red pulp (Fig. 18B). There was also a rim of positive cells just adjacent to the white pulp. No significant staining was seen when the primary antibody was omitted or when preimmune serum was used.

In vitro upregulation of AIF-1 transcripts in IFN- $\gamma$ -treated macrophages.

Expression of the T-cell-derived cytokine IFN- $\gamma$  is persistently upregulated in chronically rejecting cardiac allografts. To examine whether IFN- $\gamma$  is involved in the regulation of AIF-1 expression, in vitro stimulation studies were performed with various rodent macrophage-like cell lines or isolated macrophage populations. In these studies IFN- $\gamma$  stimulation increased AIF-1 mRNA expression in mouse J774A.1, RAW264.7, and P388D.1 cell lines, as well as in rat bone marrow-derived macrophages. The basal level of AIF-1 expression varied among the cell populations, as did the peak expression level in response to IFN- $\gamma$  stimulation (3-6-fold). In a representative study of J774A.1 cells (Fig. 19A), AIF-1 transcript levels increased significantly (5-fold) 24 h after stimulation with IFN- $\gamma$ , in comparison with cells stimulated with phorbol 12-myristate-13-acetate, LPS, or a combination of IFN- $\gamma$  and LPS ( $p < 0.0001$ ). AIF-1 transcript levels did not change significantly at 4 and

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10 h with any of the stimulants studied. A more detailed time-course study of the IFN-g response showed that the increase in AIF-1 transcripts was delayed, peaking in J774A.1 cells at 36 h after stimulation (Fig. 19B). The most effective dose of IFN-g was 100 units per ml of medium (Fig. 19C). This late increase in AIF-1 gene expression suggests that its upregulation by IFN-g may be an indirect effect.

In vivo modulation of T-cell activation reduces AIF-1 transcripts in cardiac allografts.

To study the regulation of AIF-1 expression in vivo, strategies that attenuate T-cell activation and reduce IFN-g expression were utilized. Modulation of the inflammatory response with an EFAD diet decreases expression of IFN-g at day 28, reduces mononuclear cell infiltration, and attenuates arteriosclerotic development in Lewis to F344 cardiac allografts. AIF-1 transcript levels in 28-day cardiac allografts from recipients on the EFAD diet were reduced significantly in comparison with those in allografts from recipients fed a control diet ( $p < 0.0001$ ) (Fig. 10A). In contrast, at day 7 (before the EFAD diet has any effect), there was no significant difference in AIF-1 transcript levels in allografts on the EFAD diet versus the control diet. AIF-1 transcript levels in host hearts were uniformly low.

In addition, blocking the CD28/B7 costimulatory pathway of T-cell activation with CTLA-4 Ig appears to prolong allograft survival and prevent T-cell and macrophage activation in the Lewis to F344 rat model Sayegh et al., supra. AIF-1 transcript levels were reduced significantly in cardiac allografts from recipients treated with CTLA-4 Ig, in comparison with untreated allografts or cyclosporine A-treated (single dose on day 2) allografts ( $p < 0.0001$ ) (Fig. 10B). The



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most dramatic decrease was seen in the group that received CTLA-4 Ig in addition to donor cells on the day of engraftment. AIF-1 transcript levels in this group were significantly lower than those in cardiac allografts that received CTLA-4 Ig alone ( $p < 0.0001$ ), and similar to those seen in control syngrafts. Taken together, these observations suggest that AIF-1 levels in cardiac allografts are regulated directly by T-cell activation or by cytokines secreted after activation, as suggested by the in vitro data showing that the T-cell-derived cytokine IFN- $\gamma$  upregulated AIF-1 expression.

EXAMPLE 5: Human AIF-1

Human AIF-1 cDNA was cloned and characterized as described below.

15 Materials and methods.

Human endomyocardial specimens for RT-PCR analysis were obtained from heart transplant recipients in conjunction with those obtained for routine surveillance. All tissues were harvested after obtaining informed consent under a protocol approved by the subcommittee on human studies. Routine histologic assessment completed by the staff pathologists using the International Society for Heart Transplantation (ISHT) criteria showed that all four specimens had no evidence of rejection (ISHT grade 0/4). Endomyocardial samples were quick frozen in liquid nitrogen and stored at -70 C until RNA extraction was performed.

Human inflammatory and hepatoma cell lines were obtained from the ATCC and cultured according to their recommendations. Human umbilical vein endothelial cells and umbilical artery smooth muscle cells were obtained from Cell Systems (Kirkland, WA), and cultured according to their recommendations. Human interferon gamma (Promega) (100u/ml) was added to the cell cultures for 24

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hours prior to harvest. Human heart tissue was obtained from the explanted heart at the time of transplantation.

Total RNA was isolated from tissue samples or cells maintained in tissue culture using RNazol B (Teltest, Inc. , Friendswood, TX). The quality of the total RNA was evaluated by electrophoresis through denaturing agarose gels. cDNA synthesis was completed with random primers (Gibco-BRL, Gaithersburg, MD) as recommended by the manufacturer. The success of the cDNA synthesis was evaluated by amplification of a reference gene,  $\beta$ -2-microglobulin (B2M) (forward primer: 5-CTC GCG CTA CTC TCT CTT TCT GG (SEQ ID NO: 37) and backward primer: 5'-TTA AGT GGG ATC GAG ACA TGT AAG C (SEQ ID NO: 38)) (Clontech, Palo Alto). In the initial PCR amplification of AIF-1 transcripts from human endomyocardial biopsies, primers selected from the coding region of the rat cDNA (Accession number U179179) were used (forward primer: 5'ATC CCA AGT ACA GCA GTG ATG AGG (SEQ ID NO: 35) and backward primer 5'GTC CCC CAG CCA AGA AAG CTA TTT (SEQ ID NO: 36)) to amplify a predicted 329 bp PCR product. Amplification was completed for 32 cycles with these primers. PCR reagents and reaction conditions were as described above. In brief, parameters included denaturation at 94°C for 15 sec, annealing at 56°C for 20 sec, and extension for 60 sec (with a final extension of 7 min). PCR products were separated on agarose gels. For Southern analysis, PCR products were denatured and transferred to nitrocellulose by standard capillary transfer techniques. The blots were hybridized with oligonucleotides from a sequence specific to human AIF-1 nested between the region defined by the primers used for PCR (5'-TGA GAA AGT CAG GGT AGC T; SEQ ID NO: 39). The oligonucleotide was <sup>32</sup>P end-labeled using T4 polynucleotide kinase (Promega, Madison, WI). The blot was washed with 3 x SSC, 0.1% SDS and 0.05% sodium

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pyrophosphate at 42°C, and exposed to Kodak X-omat AR film.

The initial characterization of the rat AIF-1 cDNA revealed alignment with genomic sequences within the human HLA class III region termed BAT-2, as described above. Given that the preliminary screen completed with primers from the rat sequence showed that AIF-1 transcripts were present in human biopsies, primers corresponding to these HLA class III sequences were selected. This permitted the specific amplification of the human AIF-1 cDNA coding region. In subsequent PCR analyses, primers specific for human AIF-1 cDNA were employed (forward primer 5'-ACC TCT ACC AGC ATC TGC (SEQ ID NO: 40) and backward primer 5'-TGA AGG GAA AAG GGA TGA TGG (SEQ ID NO: 41)), resulting in a 489 bp product. Amplification was performed for 29 cycles.

The PCR products amplified from cDNAs obtained from THP-1 cells and two of the human endomyocardial biopsies were cloned directly into the TA cloning vector (Invitrogen) and sequenced (United States Biochemicals). Sequence alignments were performed using the McVector and the GCG software package.

Human heart allografts were obtained as previously described (Lin et al., J. Heart Lung Transplant. 13:824-833, 1994). In brief, human allografts were collected as soon as possible after explant or autopsy, immersed in RPMI 1640, rinsed in PBS, and weighed. Ventricular sections were taken immediately and frozen in OCT. Serial cyrostat sections (4 µM) were stained, employing a Ventana automated immunostainer (Ventana Inc., Palo Alto, CA. Protein A-purified polyclonal rabbit anti-sera against rat AIF-1 (1:100 dilution) was employed as the primary antibody. To identify macrophages, MAb KP1 (Dako Incorporated) directed against CD68 was employed. The

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primary antibody was omitted in the negative control sample.

### Results

In order to determine whether AIF-1 gene transcripts were present in endomyocardial biopsies from human cardiac allografts, RT-PCR amplification was performed using primers derived from rat AIF-1. As shown in Fig. 21A, AIF-1 gene transcripts from cDNAs obtained from four separate patients (lane 3-6) as well as the control day 28 rat cardiac allograft (lane 2) were amplified. Fig. 21B shows amplified products using beta 2-microglobulin as a reference gene for the human samples. There was concordance in the intensities for AIF-1 and B2M PCR products, suggesting that the variability reflects differences in the RNA or cDNA loading the reactions. The identity of these PCR fragments was confirmed by Southern analysis (Fig. 21C). Intense hybridization is seen using a <sup>32</sup>P-oligonucleotide probe corresponding to sequences internal or nested between the original primers. Similar findings were obtained in analysis of an additional six biopsies. These findings confirm the presence of AIF-1 transcripts in human as well as rat cardiac allografts.

In order to clone the human AIF-1 cDNA, PCR primers from the HLA class III genomic region were designed to amplify the fragment corresponding to the rat open reading frame. PCR amplification using cDNAs from human myeloid cell lines THP-1, U937, and HL-60 revealed single bands corresponding to 489 bp. Sequence analysis showed 86% identity between the rat and human fragments at the nucleotide level. Comparison of the deduced amino acid sequences within the coding region (Fig. 22; SEQ ID NOs: 5 and 42) revealed 90% identity and 95% similarity between the human and rat. The identity was confirmed

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between the available sequences for U937, THP-1, and two human biopsies. Furthermore, the human AIF-1 cDNA aligns with genomic sequences in the HLA Class III region. Nucleotide and predicted amino acid sequence searches of  
5 the GenBank (release 85.0) and EMBL (release 36.0) data bases showed no alignment with any reported coding sequences.

Immunostaining confirmed the presence of the AIF-1 gene product in human cardiac allografts. AIF-1 positive  
10 cells were identified in all of the frozen sections from the four transplant patients examined. The AIF-1 antigen localized exclusively to mononuclear cells (typically in clusters) found in the interstitium and perivascular space, as seen in the representative low power (Fig. 23A)  
15 and high power (Fig. 23B) sections. The AIF-1 positive cells are most likely macrophages, given that in seriate sections they localize to regions rich in macrophages identified using the human macrophage marker KP-1 (directed against CD68) (Figs. 23C and 23D). Similar to  
20 the rat immunocytochemical studies discussed above, the anti-AIF-1 anti-serum produces a cytoplasmic staining pattern in human mononuclear cells. Interestingly, the AIF-1-positive cells represent only some of the  
infiltrating macrophage population in the transplanted  
25 heart, suggesting that this subset represents a distinct population, perhaps activated or differentiated by local factors.

Human AIF-1 gene expression patterns in various cell types were evaluated using RT-PCR assay to compare  
30 relative AIF-1 gene transcript levels. Amplification of the control gene ( $\beta_2M$ ) was successful in all cases (lower panels of Figs. 24A and B). As seen in the representative gel in Fig. 24A, AIF-1 transcripts are present solely in the cDNA derived from human macrophage-  
35 like cell lines (THP-1 (lane 1), U937 (lane 2) and HL-60

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(lane 3)). T-cell lines MOLT-4 (lane 4) and Jurket (lane 5), HepG2 (lane 6), human umbilical vein endothelial cells (HUVEC; lane 7), and human umbilical artery smooth muscle cells (HSCM; lane 8). AIF-1 transcripts were also amplified to variable degrees in six endomyocardial biopsies from human cardiac allografts (Fig. 24B).

#### EXAMPLE 6: Rat AIF-2

As stated above, the differential display screening method of the invention identified a second novel gene, designated AIF-2. The 2.2-kb cDNA fragment of AIF-2 identified up to 3 transcripts (1.5 bp, 3.5 bp, >8.0 kb) in various rat cardiac allografts (day 7, 14, 28) and spleens (but not in the other 8 organs examined). Gene transcript levels measured by reverse transcription PCR indicated that AIF-2 was found in inflammatory cells enriched in macrophages (adherent splenocytes, peritoneal macrophages, a rat pulmonary alveolar macrophage cell line, and bone-marrow macrophages). Preliminary studies indicated that transcript levels in bone-marrow macrophages increased after stimulation with interferon-gamma (IFN- $\gamma$ ) alone or with the combination of IFN- $\gamma$  and lipopolysaccharide (LPS).

The full-length AIF-1 cDNA (SEQ ID NO:4) was found to be 627 bp in length and contain a 70-bp 5' untranslated region, a continuous open reading frame (longest open reading frame 441 bp), and a 140-bp 3' untranslated region that included one potential polyadenylation sequence. The first ATG was located at base 71. Translation of the open reading frame predicted a 147-amino acid polypeptide with a predicted molecular mass of 16.8 kDa. Charged amino acids comprised 35% of the predicted polypeptide without any cysteines. A hydrophilic profile was predicted from the plot generated using the Kyte and Doolittle algorithm. This plot

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revealed the absence of any hydrophobic stretches, suggesting that AIF-1 is not a membrane-spanning protein.

Only partial cDNAs derived from the 3' end of the gene have been obtained for AIF-2 (see SEQ ID NOs:2,3,8-5 27). The remaining 5' sequences can be obtained with further screening of the cardiac allograft library, using known methods employing probes derived from the previously cloned and sequenced 3' fragments. In addition to further screening of the library, PCR 10 amplification of 5' cDNA ends can be accomplished using 5'-RACE (Rapid Amplification of cDNA ends)-Ready™ cDNA and the 5' AmpliFINDER™ RACE Kit from Clontech, Inc. Using this cloning strategy, random hexamers are used for cDNA synthesis, followed by ligation of a modified 15 single-stranded anchor oligonucleotide to the 3' end of the first-strand cDNA. Nested AIF-2 primers derived from the 3' end of the gene and a 5' primer complementary to the anchor can then be used to progressively amplify the remaining 5' end of the gene.

#### 20 Clinical applications

As described above, measurements of gene transcript or polypeptide product levels may serve as clinical or diagnostic indicators of macrophage infiltration, chronic inflammation, transplant rejection, 25 and other forms of arteriosclerosis such as atherosclerosis. AIF-1 may be used to identify subsets of macrophages, given that *in situ* hybridization and immunohistochemical studies show that AIF-1 is expressed by only some of the macrophages in the cardiac allograft 30 and in human atherosclerotic plaques. All or part of the DNAs of the invention, e.g., AIF-1 DNA with the sequence of SEQ ID NO: 1 or 4 or the AIF-2 DNA with the sequence of SEQ ID NO:2, 3, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27, can be used as 35 hybridization probes to identify AIF-1 or AIF-2,

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respectively, for the purpose of diagnosing transplant rejection. Portions of these DNAs can also be used as PCR primers to amplify AIF-1 or AIF-2 sequences to identify expression of these genes in allografts for the purpose of diagnosing rejection. The DNA of SEQ ID NO: 1 or 4 can also be used as a reliable transcriptional marker for macrophages.

Administration of AIF-1 or AIF-2 polypeptides or antibodies which bind to either AIF-1 or AIF-2 may modulate the inflammatory response by blocking cell infiltration, migration, activation, or macrophage effector functions. Macrophages have a broad number of effector functions (antigen presentation, parasitic and viral killing, phagocytosis, tumor clearance) which could be impaired by blocking AIF-1 or AIF-2. All or part of the DNAs of the invention, e.g., AIF-1 DNA with the sequence of SEQ ID NO: 1 or 4 or the AIF-2 DNA with the sequence of SEQ ID NO: 2, 3, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27, can be cloned into an expression vector and used to produce polypeptides of AIF-1 or AIF-2 for the purpose of immunizing animals to generate polyclonal or monoclonal antibodies. Such antibodies can then be used for therapeutic applications as described above or for diagnostic applications such as identification of AIF-1 or AIF-2 polypeptides in allografts indicating ongoing transplant rejection.

Also, fusion proteins of AIF-1 or AIF-2 containing components known to block specific inflammatory factors (see Other Embodiments) may also serve as a way of modulating the inflammatory response.

In addition to these therapeutic applications, valuable animal models to study allograft rejection can be made by producing transgenic animals (e.g., mice, rats, rabbits, guinea pigs, hamsters, dogs, goats,



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horses, cows, pigs, or sheep) in which the genes encoding AIF-1 or AIF-2 are deleted or overexpressed using methods known in the art. Such transgenic animals could serve as models of an impaired inflammatory response for research studies aimed at elucidating the pathophysiologic process.

EXAMPLE 7: Characterization of Gal/GalNAc macrophage lectin as a mediator of transplant rejection

Disclosed herein is the first demonstration of an *in vivo* role of Gal/GalNAc macrophage lectin in a pathologic state—chronic cardiac rejection. Of particular interest is the unique localization of the expressed gene to the allograft, a degree of compartmentalization not heretofore reported in rejecting organs. By also demonstrating the upregulation of Gal/GalNAc macrophage lectin in association only with inflammatory macrophages elicited with thioglycolate, the data detailed below further substantiate that local activation of inflammatory cells plays a role in the phenomenon of chronic rejection. Taken together, these findings suggest that Gal/GalNAc macrophage lectin, a marker of inflammatory macrophages, is likely to be one of the factors that mediate the recruitment or adhesion of macrophages in chronic cardiac rejection.

Lectins are a family of cell-surface proteins that specifically and selectively bind to complex carbohydrates on apposing cells (Sharon, N. and H. Lis., 1989, Lectins as cell recognition molecules, *Science*, 246:227-234). They have emerged as primary markers for cell recognition with clear functional roles. For example, interference with a lectin's binding to its apposing carbohydrate can disrupt bacterial and mononuclear cell attachment, tumor metastasis, and embryogenesis. Gal/GalNAc macrophage lectin falls into the category of C-type animal lectins characterized by

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calcium-dependent activity, extracellular location, and absence of free thiols. The murine lectin has been purified in an effort to identify the factor responsible for the tumor binding capacity it conferred to murine macrophages after stimulation with the antitumor streptococcal preparation OK-432 (Oda et al., 1988, *supra*; Oda et al., 1989, *supra*). Antibody against the murine lectin prevented macrophage binding to and killing of tumor cells. Kawasaki et al. cloned rat macrophage lectin, which these researchers designated macrophage-asialoglycoprotein-binding protein (m-ASGP-BP), and performed comparisons with the extensively studied rat hepatic lectins (RHL) (Ii et al., *supra*; Kawasaki, T., M. Ii, Y. Kozutsumi, and I. Yamashina, 1986, Isolation and characterization of a receptor lectin specific for galactose/N-acetylgalactosamine from macrophages, *Carbohydr. Res.*, 151:197-206; Ii, M., T. Kawasaki, and I. Yamashina, 1988, Structural similarity between the macrophage lectin specific for galactose/N-acetylgalactosamine and the hepatic asialoglycoprotein binding protein, *Biochem. Biophys. Res. Commun.*, 155:720-725). Single-chain m-ASGP-BP was shown to form homooligomeric receptors that bind and internalize ligand in a high-affinity fashion specific for Gal and GalNac (Ozaki, K., M. Ii, N. Itoh, and T. Kawasaki, 1992, Expression of a functional asialoglycoprotein receptor through transfection of a cloned cDNA that encodes a macrophage lectin, *J. Biol. Chem.*, 267:9229-9235). Rat hepatic lectin is an endocytic receptor for deglycosylated serum glycoproteins. The major form, RHL1, has a 59% homology with the macrophage lectin cDNA. The 2 minor forms, RHL2 and -3, have 45% homologies. An interesting variation in the macrophage lectin protein is the 24 amino-acid insertion that includes an Arg-Gly-Asp or RGD sequence. RGD is an integrin recognition

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sequence, raising the possibility that Gal/GalNAc macrophage lectin also confers integrin mediated cellular adhesion.

Mechanisms regulating monocyte/macrophage recruitment are of great interest in understanding pathophysiologic processes (Valente, A.J., M.M. Rozek, E.A. Sprague, and C.J. Schwartz, 1992, Mechanisms in intimal monocyte-macrophage recruitment. A special role for monocyte chemotactic protein-1, *Circulation*, 86:III-20-III-25). A spectrum of cell-surface molecules or receptors is believed to control macrophage function. For example, cytokine receptors, such as the receptor for interferon- $\gamma$ , modulate the activation of macrophages; integrin receptors, such as CD11a/CD18, regulate integrin adhesion; and the mannose receptor, a macrophage lectin, is involved in endocytosis. Gal/GalNAc macrophage lectin may also fall into this category, given that it is specifically and locally upregulated in the context of a pathophysiologic process where the hallmark is monocyte/macrophage infiltration and arteriosclerosis. More studies are required to identify the functional role of Gal/GalNAc macrophage lectin and to clarify the carbohydrate ligand on apposing cells such as allograft cells. By analogy with other lectins, it is possible that Gal/GalNAc macrophage lectin is also involved in the recognition of macrophages by exposed carbohydrates, and in their localization or adhesion to injured or stimulated donor tissue.

Differentially expressed Gal/GalNAc macrophage lectin

Analysis of polyacrylamide gels containing randomly amplified PCR products obtained by using OPA 4 (AAT CGG GCT G) (SEQ ID NO: 29) as a 5' primer and T<sub>12</sub>VTC (where V included A, C, and G) as a 3' primer identified an ~380-bp fragment in sample lanes from allogeneic hearts but not in those from syngeneic hearts (Fig. 1A).

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When the cDNA in these upregulated bands was harvested, reamplified, and used to probe Northern blots, an allograft-specific hybridization pattern was visible (Fig. 1B). Transcripts of 1.4 kb were identified in lanes 3 through 6, containing total RNA derived from 4 hearts after allogeneic transplantation, but not in lanes 1 and 2, containing RNA from 2 syngeneic transplants. RNA loading prior to transfer is shown in the ethidium-stained agarose gel (Fig. 1C). These findings confirmed the gene regulation pattern identified in the differential mRNA display analysis performed with the same panel of total RNAs. Northern analysis was then completed with total RNA obtained from an additional 6 allogeneic transplantations (3 each harvested at 7 and 14 days) and 2 syngeneic transplantations (both harvested at 14 days). Fig. 2 shows a strong hybridization to 1.4-kb transcripts in all 6 lanes (lanes 5-7 and 14-16) containing allografted heart samples, in contrast with the 6 paired host-heart samples and 4 syngeneic-heart samples (2 hosts and 2 syngrafts). Taken together (Figs. 1 and 2), these findings indicate that the induction was not restricted to individual animals or procedures but occurred uniformly in Lewis to F344 cardiac transplantation.

25 Cloning of Gal/GalNAc macrophage lectin from a rat cardiac cDNA library

Direct cloning of the amplified PCR fragment harvested from the differential display gel produced a 380-bp insert. When this insert was used as a probe in Northern blot analysis, it hybridized to transcripts of 1.4-kb (data not shown) in lanes containing RNA from cardiac allografts but not in lanes containing samples from the host hearts, again reproducing the pattern identified by the differential display analysis. To determine the identity of the full-length cDNA, a cardiac allograft cDNA library (Stratagene, La Jolla, CA) was

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screened with the 380-bp cloned PCR fragment. Nine recombinants were identified, the largest of which was 1.4 kb. Sequence analysis of this fragment and homology searching revealed that the fragment was 99% homologous to rat Gal/GalNAc-macrophage lectin mRNA (GenBank accession number J05495). The J05495 cDNA had been cloned from a rat peritoneal macrophage cDNA library.

Characterization of Gal/GalNAc macrophage lectin gene expression with a full-length cDNA clone

10 Northern blot analysis was used to examine the specificity of Gal/GalNAc macrophage lectin gene expression in a variety of rat organs, particularly those known to contain various resident mononuclear cells. Probing with full-length Gal/GalNAc macrophage lectin cDNA, strong hybridization was observed only in lane 2 containing RNA from the 28-day cardiac allograft (Fig. 3). A sample from the host spleen (lane 3) was included in the assay to determine whether Gal/GalNAc macrophage lectin transcripts were induced by a systemic effect on macrophages after transplantation. The sample from the spleen of a rat 8 hours after intraperitoneal treatment with lipopolysaccharide (lane 4) was included to determine whether this potent inflammatory stimuli would alter Gal/GalNAc macrophage lectin expression in the spleen. A control spleen sample (lane 5) harvested without any stimulation was also included. All 3 samples from spleens showed faint to no hybridization, even though spleens are the principal source of macrophages. Similarly, hybridization signals were not apparent in the lanes containing RNA from other organs including the liver (lane 6), which contains Kupffer cells, lung (lane 7), which contains alveolar macrophages, kidney (lane 8), adrenal gland (lane 9), ovary (lane 10), testes (lane 11) and skeletal muscle (lane 12). This restricted pattern of Gal/GalNAc macrophage lectin expression suggests that

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its induction is specific to and localized within the cardiac allograft.

Reverse-transcription PCR measurement of Gal/GalNAc macrophage lectin transcript levels

5 To achieve greater sensitivity in measuring Gal/GalNAc macrophage lectin transcripts, a reverse transcription-PCR assay was developed using specific primers. PCR conditions were established to insure a linear amplification rate to avoid an amplification  
10 plateau in which the PCR product level is no longer proportional to the starting template level. Gal/GalNAc macrophage lectin gene amplification (Fig. 4) was linear over 8 PCR cycles (upper panel) and by more than 2 logs in initial template or cDNA concentration (represented as  
15 the calculated amount of cDNA in the PCR reaction) (lower panel). These ranges are consistent with those typically found in PCR assay systems. For subsequent comparisons of Gal/GalNAc macrophage lectin gene transcript levels in various sets of cDNAs, PCR amplification of the control  
20 gene, G3PDH, was performed to derive corrected or normalized levels. This approach was used to compare relative differences between samples from three separate cDNA panels.

Specific and localized increase in corrected Gal/GalNAc macrophage lectin levels in cardiac allografts

25 Fig. 5 shows that corrected Gal/GalNAc macrophage lectin gene transcript levels increased significantly in cardiac allografts (black bars) at all time points studied (day 7, 14, 28, and 75) in comparison with the 3  
30 reference groups: a day-0 heart (black bar), paired host hearts (hatched bars) and a syngraft (stippled bar) ( $P < 0.008$ ). Differences in transcript levels between the various allograft time points were not significant. This lack of a difference suggests that there was no further  
35 increase after the initial induction, which would be consistent with an ongoing or chronic stimulation. To

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examine whether Gal/GalNac macrophage lectin gene induction was systemically or locally regulated, levels in cardiac allografts were compared with those in host spleens (given that the spleen would be a major source of macrophages but free of direct exposure to stimuli in allografted tissue). As seen in Fig. 6, Gal/GalNac macrophage lectin levels increased significantly in the 7- and 28-day cardiac allografts (black bars) relative to host spleens and hearts (hatched bars) ( $P < 0.0001$ ). The low transcript levels in the host spleens suggest that Gal/GalNac macrophage lectin gene induction in the cardiac allograft is due to local activation or stimulation.

15 Corrected Gal/GalNac macrophage lectin transcript levels in isolated inflammatory macrophages

Transcript levels were measured in various types of isolated rat inflammatory cells to confirm the macrophage-specific nature of Gal/GalNac gene expression. Fig. 7 shows that corrected transcript levels increased significantly in thioglycolate-elicited macrophages and cells from a 14-day cardiac allograft ( $P < 0.0001$ ) compared with adherent (macrophage-enriched) splenocytes (stimulated with buffer, concanavalin A, and lipopolysaccharide/interferon- $\gamma$ ) and nonadherent (lymphocyte-enriched) splenocytes (stimulated with buffer, concanavalin A and lipopolysaccharide/interferon- $\gamma$ ). The identification of Gal/GalNac macrophage lectin gene transcripts only in thioglycolate-elicited rat macrophages, an inflammatory macrophage population, extends the observation that antibody against the murine lectin binds only to stimulated murine macrophages (Oda, S., M. Sato, S. Toyoshima, and T. Osawa, 1988, Purification and characterization of a lectin-like molecule specific for galactose/N-acetyl-galactosamine from tumoricidal macrophages, *J. Biochem. (Tokyo)*, 104:600-605).

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In situ localization of Gal/GalNAC macrophage lectin mRNA in cardiac allografts

In situ hybridization was performed to localize the cell types expressing Gal/GalNAC macrophage lectin transcripts in cardiac allograft tissue. Positive hybridization with the antisense Gal/GalNAC probe was visible in scattered mononuclear cells within inflammatory infiltrates in the interstitium and perivascular space (Fig. 8A and 8B), as demonstrated by the clustering of silver grains (arrows). There was little hybridization to adjacent noninflammatory cells such as cardiac myocytes, or when the negative control, sense Gal/GalNAC probe (Fig. 8C and 8D) was used in serial sections. There was no significant hybridization of either the antisense or sense probe to paired host hearts, which lacked inflammatory infiltrates (not shown).

Restricted upregulation of Gal/GalNAC macrophage lectin

The gene transcripts of Gal/GalNAC macrophage lectin were found to be specifically localized to and upregulated within Lewis to F344 rat cardiac allografts. Increases in Gal/GalNAC macrophage lectin gene transcript levels occurred early (by 7 days) during initial macrophage accumulation and were sustained (through 14, 25 28, and 75 days), as would be expected for a chronic inflammatory state characterized by ongoing macrophage infiltration. In contrast, transcript levels were low in 3 reference groups: paired host hearts (exposed to the same circulation but normal on histologic examination), day-14 Lewis syngrafts (subject to the same surgical procedure but with matching host and recipient strains), and day-0 Lewis hearts (harvested but not transplanted). Furthermore, the induction of Gal/GalNAC macrophage lectin gene transcripts occurred in a compartmental fashion restricted to the allografted tissue. Transcript elevation was not found in the matching host spleens



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(studied because they are the principal source of macrophages but not subject to allogeneic stimulation), nor was it found in other organs rich in resident macrophages. This pattern is in keeping with the

5 arteriosclerotic changes found in cardiac transplants, which affect donor vessels but spare host vessels. Using *in situ* hybridization, a subset of inflammatory cells (presumably macrophages) within the cardiac allograft was shown to express Gal/GalNAc macrophage lectin

10 transcripts. In examining the specificity of Gal/GalNAc macrophage lectin gene expression in various isolated rat inflammatory cells, transcripts were found to be present only in exudative or thioglycolate-elicited macrophages. Taken together, these results show that Gal/GalNAc

15 macrophage lectin gene expression is restricted *in vivo* to a subset of infiltrating inflammatory cells in cardiac allografts and *in vitro* to inflammatory macrophages, suggesting that this lectin is an inducible factor under tight regulatory control.

20 Gal/GalNAc macrophage lectin is of particular importance in chronic rejection because *in vitro* studies suggest that its surface expression increases markedly on activated macrophages, and that it regulates the binding to and destruction of tumor cells by macrophages (Oda,

25 S., M. Sato, S. Toyoshima, and T. Osawa, 1989, Binding of activated macrophages to tumor cells through a macrophage lectin and its role in macrophage tumoricidal activity, *J. Biochem. (Tokyo)*, 105:1040-1043). These data raise the possibility that Gal/GalNAc macrophage lectin may

30 also play a role in the vascular changes that occur in chronic cardiac rejection by regulating the infiltration of macrophages within the allografts.

Cloning human Gal/GalNAc macrophage lectin

The existence of a human homologue was suggested

35 by Southern analysis using digested human genomic DNA

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which demonstrated cross hybridization with the rat Gal/GalNac macrophage lectin cDNA. The human Gal/GalNac macrophage lectin cDNA can be cloned as follows:

- Using primers derived from the rat Gal/GalNac
- 5 macrophage lectin DNA sequence, a PCR product would be amplified from human cardiac transplant biopsy tissue. The human PCR product would then be isolated and used as a template for PCR reactions using a different 5' primer based on the rat sequence and the same 3' primer.
- 10 DNA fragments derived from the rat Gal/GalNac macrophage lectin cDNA sequence or PCR fragments amplified from the human template can be used as hybridization probes to screen for overlapping cDNA inserts in a cDNA library prepared from cells previously
- 15 determined, e.g., by Northern blot, to express transcripts which bind to rat probes. The screening of cDNA libraries with radiolabelled cDNA probes is routine in the art of molecular biology (see Sambrook et al., 1989, *Molecular Cloning: a Laboratory Manual*, second
- 20 edition., Cold Spring Harbor Press, Cold Spring Harbor, N.Y).

- The human cDNA can be isolated and subcloned into a plasmid vector (e.g., pBluescriptII), and the plasmid
- 25 DNA purified by standard techniques. The cDNA insert can be sequenced using the dideoxy chain termination method well known in the art (Sambrook et al, *supra*). Oligonucleotide primers corresponding to bordering vector regions as well as primers prepared from previously isolated cDNA clones can be employed to progressively
- 30 determine the sequence of the entire gene.

- DNA containing a sequence that encodes part or all of the amino acid sequence of Gal/GalNac macrophage lectin can be recloned into an expression vector, using a variety of methods known in the art. For example, a
- 35 recombinant polypeptide can be expressed as a fusion

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protein with maltose binding protein produced in *E. coli*. Using the maltose binding protein fusion and purification system (New England Biolabs), the cloned human cDNA sequence can be inserted downstream and in frame of the  
5 gene encoding maltose binding protein (malE), and the malE fusion protein can then be overexpressed. In the absence of convenient restriction sites in the human cDNA sequence, PCR can be used to introduce restriction sites compatible with the vector at the 5' and 3' end of the  
10 cDNA fragment to facilitate insertion of the cDNA fragment into the vector. Following expression of the fusion protein, it can be purified by affinity chromatography. For example, the fusion protein can be purified by virtue of the ability of the maltose binding  
15 protein portion of the fusion protein to bind to amylose immobilized on a column.

To facilitate protein purification, the pMalE plasmid contains a factor Xa cleavage site upstream of the site into which the cDNA is inserted into the vector.  
20 Thus, the fusion protein purified as described above can then be cleaved with factor Xa to separate the maltose binding protein from recombinant human cDNA gene product. The cleavage products can be subjected to further  
chromatography to purify recombinant macrophage lectin  
25 from the maltose binding protein.

The purified recombinant gene product can then be used to raise polyclonal or monoclonal antibodies against the human macrophage lectin using well-known methods (see Coligan et al., eds., *Current Protocols in Immunology*,  
30 1992, Greene Publishing Associates and Wiley-Interscience). To generate monoclonal antibodies, a mouse can be immunized with the recombinant protein, and antibody-secreting B cells isolated and immortalized with a non-secretory myeloma cell fusion partner. Hybridomas  
35 are then screened for production of lectin-specific

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antibody and cloned to obtain a homogenous cell population which produces a monoclonal antibody.

Identification of compounds which inhibit allograft rejection

- 5 A screening method for identifying compounds capable of inhibiting the association of Gal/GalNAC macrophage lectin with its carbohydrate ligand may be carried out as follows:
- A cell which expresses Gal/GalNAC macrophage
- 10 lectin is provided. The cell is most preferably a macrophage, e.g., cell lines, such as J744A.1 (ATCC T1B67) or RAW264.7 (ATCC T1B71) for murine studies, or primary cells such as bone marrow derived macrophages, but may be any type of cell which expresses Gal/GalNAC
- 15 macrophage lectin on its surface (e.g., a cell transfected with a cDNA encoding the lectin). Alternatively, Gal/GalNAC lectin may be provided immobilized, e.g., linked to an agarose or acrylamide bead. The lectin is incubated in the presence of a
- 20 candidate compound. A reference point could be established under standard conditions and the results from any assay compared to the pre-established standard as the control. The lectin is then allowed to bind to
- 
- 25 washed to remove unbound ligand. The complexes can then be recovered, and subjected to SDS-PAGE. A reduction in the amount of label associated with the complex in the presence of candidate compound compared to that in the absence of candidate compound (or compared to a pre-
- 30 established standard) indicates that the candidate compound inhibits Gal/GalNAC macrophage lectin-mediated allograft rejection.

An in vitro binding assay may also be accomplished as follows. Modifications of the frozen section assay

35 originally described by Stamper and Woodruff (Stamper, et al., 1977, *J. Immunol.*, 119:772-780, Butcher, et al.,

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1979, *J. Immunol.*, 123:1996-2003, herein incorporated by reference), can be used to study the role of Gal/GalNAc macrophage lectin in adhesion to rat cardiac allografts. Inflammatory cells demonstrated to express the lectin

5 such as thioglycolate-elicited peritoneal macrophages or T cell-stimulated bone marrow derived macrophages (Gessl, et al., 1989, *J. Immunol.*, 142:4372-4377), herein incorporated by reference) can be labeled with the fluorescent dye 1,1'-dioctadecyl-3,3,3,3'-

10 tetramethylindocarbocyanine percholate. Labeled macrophages can be incubated with frozen tissue sections from rat cardiac allografts. Conditions can be optimized to maximize specific calcium dependent adhesion to the allograft and control heart sections by variation in

15 temperature, incubation buffer, and washing. Adherent cells can be quantitated using methods known in the art. Specificity of the adherence can be evaluated by measuring the extent of inhibition with a given candidate compound, such as, anti-lectin antibody, Gal-bovine serum

20 albumin (BSA) or GalNAc-BSA conjugates, or recombinantly expressed or modified Gal/GalNAc macrophage lectin polypeptides.

Screening for inhibitors can also be accomplished ~~in vivo~~. For example, the organ to be allografted can be

25 perfused or soaked in a solution containing a candidate compound prior to transplantation. The organ can then transplanted and monitored for indications of rejection. Transplant rejection can be monitored using conventional methods, e.g., sacrifice of the animal followed by gross

30 examination of the tissue and histological studies, as well as the diagnostic assays of the invention, e.g., evaluating a tissue biopsy for the differential expression of an allograft gene, e.g., Gal/GalNAc macrophage lectin. A decrease in gene expression or a

35 reduction in the physical characteristics of transplant

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rejection would indicate that the candidate compound inhibits allograft rejection.

Inhibition of allograft rejection by blocking binding of Gal/GalNAc macrophage lectin to Gal/GalNAc

5       The development of inhibitors (peptides, antibodies, or, carbohydrates) that block the lectin-carbohydrate interaction could provide a means of attenuating macrophage infiltration within allografts and disrupting the associated cytokine cascades believed to  
10 be initiated by macrophage activation.

Carbohydrates such as Gal or GalNAc, as well as compounds containing Gal or GalNAc, can be used to block binding of Gal/GalNAc macrophage lectin to its ligand on the surface of cells in the allografted tissue, an event  
15 that may contribute to the eventual rejection of the allografted tissue or organ.

Soluble polypeptides and fragments thereof, e.g., polypeptide containing a carbohydrate-binding fragment of Gal/GalNAc macrophage lectin, can be used to block the  
20 association of macrophage lectin with its carbohydrate ligand.

The term "fragment", as applied to a polypeptide, herein denotes a peptide of at least 10 amino acids. The polypeptide fragments of the invention are preferably at  
25 least 20 contiguous amino acids, more preferably at least 40 contiguous amino acids, even more preferably at least 50 contiguous amino acids, and most preferably at least about 80 or more contiguous amino acids in length. Such peptides can be generated by methods known to those  
30 skilled in the art, including proteolytic cleavage of the protein, de novo synthesis of the fragment, or genetic engineering, e.g., cloning the gene or a portion of the gene encoding Gal/GalNAc macrophage lectin into an expression vector as described above.

35       Also within the invention are analogs of the above peptides. Analogs can differ from the peptides encoded

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by differentially expressed genes, e.g., Gal/GalNAc macrophage lectin or a carbohydrate-binding fragment thereof, by conservative amino acid replacements which alter the sequence but do not adversely affect the functioning of the resulting polypeptide, or by modifications which do not affect the sequence, or by both. Modifications (which do not normally alter primary sequence) include *in vivo* or *in vitro* chemical derivitization of polypeptides, e.g., acetylation or carboxylation. Also included are modifications of glycosylation, e.g., those made by modifying the glycosylation patterns of a polypeptide during its synthesis and processing or in further processing steps, e.g., by exposing the polypeptide to enzymes which affect glycosylation, e.g., mammalian glycosylating or deglycosylating enzymes.

The invention includes analogs in which one or more peptide bonds have been replaced with an alternative type of covalent bond (a "peptide mimetic") which is not susceptible to cleavage by peptidases. Where proteolytic degradation of the peptides following injection into the subject is a problem, replacement of a particularly sensitive peptide bond with a noncleavable peptide mimetic will make the resulting peptide more stable and thus more useful as a therapeutic. Such mimetics, and methods of incorporating them into polypeptides, are well known in the art. Similarly, the replacement of an L-amino acid residue with a D-amino acid residue is a standard way of rendering the polypeptide less sensitive to proteolysis. Also useful are amino-terminal blocking groups such as t-butyloxycarbonyl, acetyl, theyl, succinyl, methoxysuccinyl, suberyl, adipyl, azelayl, dansyl, benzyloxycarbonyl, fluorenylmethoxycarbonyl, methoxyazelayl, methoxyadipyl, methoxysuberyl, and 2,4,- dinitrophenyl.

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Peptides may be administered to the patient intravenously in a pharmaceutically acceptable carrier such as physiological saline. Such methods are well known to those of ordinary skill in the art. The  
5 formulations of this invention are useful for parenteral administration, such as intravenous, subcutaneous, intramuscular, intraperitoneal, and inhalation.

EXAMPLE 8: Diagnosis and treatment of vascular inflammation and resulting atherosclerosis

10 It has been discovered that AIF-1, and potentially other differentially-expressed allograft genes, are upregulated in atherosclerotic plaques unrelated to the transplant context. Thought to be attributable to the vascular inflammation and injury which are believed to be  
15 part of plaque formation, this upregulation of genes originally identified by the allograft/syngraft differential display technique described above provides a means for diagnosing the existence of an atherosclerotic or pre-atherosclerotic condition in an animal. For  
20 example, the regions of relatively high level expression of AIF-1, AIF-2, Gal/GalNAc macrophage lectin, ubiquitin, or P1 can be detected by *in situ* hybridization or  
immunostaining of a tissue biopsy sample, or by  
noninvasive imaging techniques using an Indium<sup>111</sup>-labelled  
25 antibody or ligand specific for the target molecule.

This discovery also has therapeutic implications. The therapeutic methods described above with respect to preventing allograft rejection are expected to have useful applications in the prevention of atherosclerotic  
30 plaques, whether in patients diagnosed by the above techniques, or in those generally considered to be susceptible to formation of such plaques.



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Other Embodiments

Hybrid inhibitors of allograft rejection in which a first portion that blocks lectin-carbohydrate binding, e.g., a carbohydrate-binding fragment of Gal/GalNAc macrophage lectin, is linked to a second portion which decreases macrophage-mediated destruction of transplanted tissue, can be constructed using methods known in the art. The first portion can be covalently linked to the second portion, for example, by ligating DNA encoding the first portion in frame with DNA encoding the second portion into an expression vector, and recombinantly producing the hybrid inhibitor. The first portion may be a compound which blocks Gal/GalNAc macrophage lectin binding to Gal/GalNAc, such as a carbohydrate-binding fragment of Gal/GalNAc macrophage lectin, or an antibody or antibody fragment which is lectin-specific or carbohydrate-specific. The first portion of the hybrid may also be an AIF-1 or AIF-2 polypeptide. The second portion of the hybrid can be a compound which is capable of blocking inflammatory cell (e.g., macrophage) infiltration, migration, activation, or other effector functions, such as interleukin-10, transforming growth factor  $\beta$ -1, D-mannosidase, or migration inhibition factor.

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Table 1. Analysis of cDNA fragments identified by differential mRNA display

Band	Expression pattern		Transcript Size	Sequence Homology
	Differential Display	Northern Analysis		
1	allogenic	allogenic	3.5 kb	no homology*
		allogenic	1.5 kb	no homology*
2	allogenic	allogenic	1.4 kb	rat Gal/GalNAc macrophage lectin
		nonspecific	1.0 kb	not sequenced
		nonspecific	1.8 kb	not sequenced
3	allogenic	no hybridization		
4	syngenic	no hybridization		
5	allogenic	no hybridization		
6	allogenic	no hybridization		
7	allogenic	no hybridization		
8	allogenic	no hybridization		
9	syngenic	nonspecific	1.0 kb	not sequenced
10	allogenic	nonspecific	1.6 kb	not sequenced
11	allogenic	allogenic	3.5 kb	mouse P1 protein
		allogenic	1.0 kb	mouse ubiquitin-like protein
		nonspecific	5.0 kb	not sequenced
12	allogenic	allogenic	0.7 kb	no homology

\* Single cDNA clone hybridized to transcripts of two sizes.

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TABLE 2

SEQ ID NO:1

GCTGCTGTCA TTAGAAGGTC CTCGGTCCCA CCGTGTTATA TCCACCTCCA  
ATTAGGGCAA TACAGAAATA GCTTTCCTGG CTGGGGGACC AGTTGGCTTC  
5 TGGTGTTCTT TGTTTTTCTC CTCACACATC AGAATCATT CCAAGATGGC  
AGATCTCTTG CCCAGCATCA TTCTGAGAAA GTCAGAGTAA CTGAACGTCT  
CCTCGGAGCC ACTGGACACC TCTCTAATTA ATTTCTTCAG CTCTAGATGG  
GTCTTGGGAA CCCAAGTTTC TCCAGCATTC GCTTCAAGGA CATAATATCG  
ATATCTCCAT TGCCATTTCAG ATCAACTCAT G

10

TABLE 3

SEQ ID NO. 2

ACG AGA ATA TGG CTG TAA TCT GGA GGA CAT CAT TGT TGT TCT  
GGG CCC TTC AGT GGG ATC TGC TGC TTT ACC TTC CAG AGA ATC  
15 AGC AAC CTC ATT TAC CAA GTT CAT CTG TGT GTG AGA ACG TTG  
ACT

TABLE 4

SEQ ID NO. 3

TTTTTTTTTT TTGCAGCCAT TG TAGAAGGA TACGGGAAGC ATTTATCGAA  
20 AATTCAGAC AAGAACCTCA TTCTCTAAGG GATATGAAGC CTATCTGTGT  
ACCGAAGTTA AGGCCATCAC GGACATGGGA GAAAACTTC TCAGGATGGC  
AAGATGTGCA GAGGTCAAGA TCTTCCTCCT GGTCTTGAAT ATCTGTGGAA  
GAATTCCTCC TGCTTCTAGA GATCCTGTGC TTTTCGGATG TCAACGTAGG  
GATTTGGTGA GTCAAACCTGT CTCACACACG AAGGATGAAC ATTGTGAAAT  
25 GAGGTTGCTG ATCTCTGG

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TABLE 5

SEQ ID NO. 4

	GAGGAGCCAG	CCAACACACT	GCAGCCTCAT	CGTCATCTCC	CCACCTAAGG
	CCACCAGCGT	CTGAGGAGCT	ATGAGCCAGA	GCAAGGATTT	GCAGGGAGGA
5	AAAGCTTTTG	CACTGCTGAA	AGCCCAGCAG	GAAGAGAGGT	TGGATGGGAT
	CAACAAGCAC	TTCCTCGATG	ATCCCAAGTA	CAGCAGTGAT	GAGGATCTGC
	AGTCCAAACT	GGAGGCCTTC	AAGACGAAGT	ACATGGAGTT	TGATCTGAAT
	GGCAATGGAG	ATATCGATAT	TATGTCCTTG	AAGCGAATGC	TGGAGAAACT
	TGGGGTTCCC	AAGACCCATC	TAGAGCTGAA	GAAATTAATT	AGAGAGGTGT
10	CCAGTGGCTC	CGAGGAGACG	TTCAGTTACT	CTGACTTTCT	CAGAATGATG
	CTGGGCAAGA	GATCTGCCAT	CTTGAGAATG	ATTCTGATGT	ATGAGGAGAA
	AAACAAAGAA	CACCAGAAGC	CAACTGGTCC	CCCAGCCAAG	AAAGCTATTT
	CTGAGTTGCC	CTAATTGGAG	GTGGATATAA	CACGGTGGGA	CCGAGGACCT
	TCTAATGACA	GCAGCATGGG	AAAAGAAGAA	GCAGTTGTGA	GCCAGAGTCA
15	AACTAAATAA	ATAATGCTCC	CTAGTGCAAA	AAAAAAAAAA	AAAAAAAAAA A

TABLE 6

SEQ ID NO. 5

	Met	Ser	Gln	Ser	Lys	Asp	Leu	Gln	Gly	Gly	Lys	Ala	Phe	Gly
20	Leu	Leu	Lys	Ala	Gln	Gln	Glu	Glu	Arg	Leu	Asp	Gly	Ile	Asn
	Lys	His	Phe	Leu	Asp	Asp	Pro	Lys	Tyr	Ser	Ser	Asp	Glu	Asp
	Leu	Gln	Ser	Lys	Leu	Glu	Ala	Phe	Lys	Thr	Lys	Tyr	Met	Glu
	Phe	Asp	Leu	Asn	Gly	Asn	Gly	Asp	Ile	Asp	Ile	Met	Ser	Leu
	Lys	Arg	Met	Leu	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu
25	Glu	Leu	Lys	Lys	Leu	Ile	Arg	Glu	Val	Ser	Ser	Gly	Ser	Glu
	Glu	Thr	Phe	Ser	Tyr	Ser	Asp	Phe	Leu	Arg	Met	Met	Leu	Gly
	Lys	Arg	Ser	Ala	Ile	Leu	Arg	Met	Ile	Leu	Met	Tyr	Glu	Glu
	Lys	Asn	Lys	Glu	His	Gln	Lys	Pro	Thr	Gly	Pro	Pro	Ala	Lys
	Lys	Ala	Ile	Ser	Glu	Leu	Pro							

30

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## TABLE 7

SEQ. ID NO. 6  
CACATCTTGC CATCCTGA

## 5 TABLE 8

SEQ ID NO. 7  
CATGGTGCTT GAGAACAG

## TABLE 9

## 10 SEQ ID NO. 8

GTTTAATGCA GAGAAATTTT ACCGAATAAA GACTGATCAC GCCAGGTAAG  
TATGGGTAAT GGGGAAGAAG GAGCCTGAAT CTTACGATGG AATAATTACA  
AATCAGAGAG GAATCACAAT CACAGCTCTT GGCGCAGACT GTATACCTAT  
AGTCTTTGCA GATCCTGTGA AAAAAGCATG TGGGGCTGCT CACTCGGGCT  
15 GGAAGGGCAC TTTGTTGGGC GTCGCTATGG CTACTGTGAA TGCTATGATA  
GCAGAATATG GCTGTAATCT GGAGGACATC ATTGTTGTTC TGGGCCCTTC  
AGTGGGATCT

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TABLE 10

SEQ ID NO. 9

TTTTTTTTTC TTATATATAA ATTCTAACCT TTAATGTTTA TGTAACATA  
CATGTATATG GCTATGTAAA TCTGTGGGTA TAAGTGTGGA TAGGTGTTGA  
5 AACTAGAAAG GGAACATAAA AGGGGATTGT GCAAGGGAGA ACAAACACA  
TGAGACAGGA AAGAGGGGCT TCTGCAGTGA AAGGGTACAC AAGGGGCCAG  
GGAAAGGGAG AGCGAGGGCC AGAAAAACAT GGTGCTTGAG AACAGCATAA  
GGAACCTGTA TTTATAAGGC AGTT

TABLE 11

10 SEQ ID NO. 10

CCGAGTCTCG CGTCTACCAG AGCTGCAAGA TGTCTGTGCT CCCTGGAATA  
ATTGTCCTTG TGGGACGATC CTCATGTGCC TGGTGTGCCT GCTTGCTAGT  
AGGAGGAATA ATACCGGTTT ATTCTCCTAC CGGAACACCA ATATGTATAT  
GTGCATCGGC CCAAGTCAT CATTGAAAAC ACAGTGTCTT CAAGTGGACA  
15 AGACCTTCAC TGGATTGTTC AAGAGAGATC CAGCCTTACA AGAAGGAAAA  
CTAGAGACCA AAATAAATCC TCTTCCTTCT CGATGGGTAT CATCTGCTTC  
TTCTTCCTAA AAGACTGGGG GAGCTATCTC TCATAGTGAG TACATTCAGT  
GTGCAAGTGG CTCTCAGAGT AGACTCAGTC CTTGCTTG

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TABLE 12

SEQ ID NO. 11

TCGAGTTTTT TTTTTTTTTT TTTATATATA AATTCTAACC TTTAATGTTT  
ATGTAAACAT ACATGTATAT GGCAATGTAA ATCTGTGGGT ATAAGTGTGG  
5 ATAGGTGTTG AAAC TAGAAA GGGAACATAA AAGGGGATTG TGCAAGGGAG  
AACAAAACAC ATGACAGGAA AGAGGGGCTT CTGCAGTGAA AGGGTACACA  
AGGGGCCAGG GAAAGGGAGA GCGGAGGGCC AGAAAAACAT GGTGCTTGAG  
AACAGCATAA GGAAACCTGT ATTTTATAAG GCAGTAAAAA TATACATTTA  
AAAGGAACG

10

TABLE 13

SEQ ID NO. 12

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT CTTATATATA AATTCTAACC  
TTTAATGTTT ATGTAAACAT ACATGTATAT GGCTATGTAA ATCTGTGGGT  
15 ATAAGTGTGG ATAGGTGTTG AAAC TAGAAA GGGAACATAA AAGGGGATTG  
TGCAAGGGAG AACAAAACAC ATGAGACAGG AAAGAGGGGC TTCTGCAGTG  
AAAGGGTACA CAAGGGGCCA GGGAAAGGGA GACGGAGGGC CAGAAAAACA  
TGGTGCTTGA GAACAGCATA AGGAAACCTG GTATTTTATA AGGCAGTTAA  
AAATATACAT TTAAGGAA ACGTTTATCT CCCCTACTGC ATTTGATTCA  
20 AATGAGAAGG TG

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TABLE 14

SEQ ID NO. 13

5 GAAAAAGGTG CCTGACTGAA GAATGGCAGA AGCAGTCTTG ATAGATCTCT  
CTGGTTTACA ATTGAACTCT CAGGAAAACT GTCATCAGAT GGTACTGAAG  
ACGCTGGATG GTATTCACGA CCACCATGCC CCCAAGGCCA AGTTCCTTTG  
TATAATATGT TGCAGCGATG CCACCAATGG AAAGGGTGGG GAATATGGCC  
TCTGTGAACT GGAAGCAGGA AATGGCTTTT CAAGTCTCGC GGGAAAATTC  
GAGACTGTTA GCCATCCAGC CTGGCTGCCT CTTTGTATTC AGTTAAACAA  
AAATAGATGA GGAGGATCTG AGCCGCGTTA AGGTGATTGT GCCCGAG

10

TABLE 15

SEQ ID NO. 14

15 TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT ACATACACAC  
AGTATTTTAT TTAGCCATAA TGAAATTATC AACTTATAG GAAAAATTGA  
TGGATCTGGA ATTATTTTAT ATGAGCAAAA TAATCCAGAC TCAGAATAAG  
AAACACCACA TGTTCCTTCT TATATATAAA TTCTAACCTT TAATGTTTAT  
GTAAACATAC ATGTATATGG CTATGTAAAT CTGTGGGTAT AAGTGTGGAT  
AGGTGTTGAA ACTAGAAAGG GAACATAAAA GGGGATTGTG CAAGGGAGAA  
CAAAACATAT GAGACAGGAA AGAGGGGCTT CTGTAGTGAA AGGGTACCAA

20



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TABLE 16

SEQ ID NO. 15

TCTCAGCTCA CTCAATCTTT TCAGTAGTTC CAAACGGAGA GATCCCAAAG  
5 TGGTTGTTCA AGAAAACCTC CGCGGCCTGG CAAATGCTGC AGGGTTTAAT  
GCAGAGAAAT TTTACCGAAT AAAGACTGAT CACGCCAGGT AAGTATGGGT  
AATGGGGAAG AAGGAGCCTG AATCTTACGA TGGAATAATT ACAAATCAGA  
GAGGAATCAC AATCACAGCT CTTGGCAGAC TGTATACCTA TAGTCTTTGC  
AGATCCTGTG AAAAAAGCAT GTGGGGCTGC TCACTCGGGC TGGAAGGGCA  
10 CTTTGTGGG CGT

TABLE 17

SEQ ID NO. 16

TTTTTTTTTT TTTTTTTTTT TTCTTATATA TAAATTCTAA CCTTTAATGT  
15 TTATGTAAAC ATACATGTAT ATGGCTATGT AAATCTGTGG GTATAAGTGT  
GGATAGGTGT TGAAACTAGA AAGGGAACAT AAAAGGGGAT TGTGCAAGGG  
AGAACAAAAC ACATGAGACA GGAAAGAGGG GCTTCTGCAG TGAAAGGGTA  
CACAAGGGGC CAGGGAAAGG GAGAGCGGAG GGCCAGAAAA ACATGGTGCT  
TGACAATAGC ATAAGGAAAC CTGGTATTTA TAAGGCAGTT AAAAA

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TABLE 18

SEQ ID NO. 17

TCGGGCAGGA AGGGCACTTT GTTGGGCGTC GCTATGGCTA CTGTGAATGC  
AGTGATAGCA GAATATGGCT GTAGTCTGGA GGACATCGTT GTTGTTCTGG  
5 GCCCTTCAGT GGGATCTTGC TGCTTTACTC TTCCCAGAGA ATCAGCAACC  
TCATTTTACA ATGTTTCATCC TTCGTGTGTG AGACAGTTTG ACTCACCAAA  
TCCCTGCGTT GACATCCGAA AAGCCACCAG GATTCTTCTA GAACGAGGAG  
GAATTCTTCC ACAGAATATC AAGACCAGGA GGAAGATCTG ACCTCTGCAC  
ATCTGCCATC TGAGAG

10

TABLE 19

SEQ ID NO. 18

TTTTTTTTTT TTTTTTTATA TATAAATCT AACCATTAA TGTTTACGTA  
AACATACATG TATATGGCTA TGTAATCTG TGGGTATAAG TGTGGATAGG  
15 AGTTGAAACT AGAAAGGGAA CATAAAAGGG GATTGTGCAA GGGAGAACAA  
AACACATGAG ACAGGAAAGA GGGGCTTCTG CAGTGAAAGG GTACACAAGG  
GGCCAGGGAA AGGGAGAGCG GAGGGCCAGA AAAACATGGT GCTTGAGAAC  
AGCATAAGGA AACCTGGTAT TTTATAAGGC AGTTAAAAAT ATACATTAA  
AAGGAAACGT TTATCTCCCC

20

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TABLE 20

SEQ ID NO. 19

CCGGGGCGCC GGCCGGCCGT GGCGGGAACA CCCGAACTCC GGTGCCCCGGA  
GGCCCGGACG CTGTGAGGCG GCGAGCGGG CGGACCCGTT CGGGCGACTC  
5 TGGGGTTTCGT TCCCCGAGGC TGCAGCTCAC ACCCCAGCTC GCGGCCGCCG  
AGGAGAGCGC GGGAAGCGCC CCGCGTGATT TGGCATAAAA GTCTTTGGGG  
GAAAAAGGTG CCTGACTGAA GAATGGCAGA AGCAGTCTTG ATAGATCTCT  
CTGGTTTACA ATTGAACTCT CAGGAAAAC GTCATCAGAT GGTACTGAAG  
ACGCTGGATG GTATCAC

10

TABLE 21

SEQ ID NO. 20

TTTTTTTTTT TTTTTTTTTT ACAGTACATA CACACAGCAT TTTATTTAGC  
CATAATGAAA TTATCAAAC TATAGGAAAA ATTGATGGAT CTGGAATTAT  
15 TTATTATGAG CAAAATAATC CAGTCTCAGA ATAAGAAACA CCACATGTTC  
TTTCTTATAT ATAAATTCTA ACCTTTAATG TTTATGTAAA CATAAGTAT  
ATGGCTATGT AAATCAGTGG GTATAAGTGT GGATAGGTGT TGAAACTAGA  
AAGGGAACAT AAAAGGGGAT TATCGAAGGG AGAACAAAAC ACATGAGACA  
GGAAAGAGGG GCAATAGTAG TGAAAGGGAA TATAAGGGGC CAGGG

20

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TABLE 22

SEQ ID NO. 21

5 CCTCCGCAGC TGGCAAATGC TGCAGGGTTT AATGCAGAGA AATTTTGCCG  
AATAAAGACT GATCACGCCA GGTAAGTATG GGTAAATGGG AAGAAGGAGC  
CTGAATCTTA GCATGGAATA ATTACAAATC AGAGAGGAAT CACAATCACA  
GCTCTTGGCG CAGACTGTAT ACCTATAGTC TTTGCAGATC CTGTGAAAAA  
AGCATGTGGG GCTGCTCACT CGGGCTGGAA GGGCACTTTG TTGGGCGTCG  
CTATGGCTAC TGTGAATGCT ATGATAGCAG AATATGGCTG TAATCTGGAG  
GACATCATTG TTGTTCTGGG CCCTTCAGT

10

TABLE 23

SEQ ID NO. 22

TTTTTTTTTT TTTTTTTTTT TACAGTACAT ACACACAGTA TTTTATTTAG  
CCATAATGAA ATTATCAAAC TTATAGGAAA AATTGATGGA TCTGGAATTA  
15 TTTATTATGA GCAAAATAAT CCAGACTCAG AATAAGAAAC ACCACATGTT  
CTTTACTTAT ATATAAATTC TAACCTTTAA TGTTTATGTA AACATACATG  
TATATGGCTA TGTAAATCTG TGGGTATAAG TGTGGATAGG TGTTGAAACT  
AGAAAGGGAA CATAAAACGG GGATTATGCA AGGGAGAACA AAACACATGA  
GACAGGAAAG AGGGGCTTCT G

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TABLE 24

SEQ ID NO. 23

CCTCCGCAGG CTGGCAAATG CTGCAGGGTT TGGTGTAGAG AAATTTTACC  
GAATAAAGAC TGATCATGTT AGTGAAGTAT GGGTAATGGG GAAGAAGGAG  
5 CCTGAATCTT ACGATGGAAT AATTACAAAT CAGAGAGGAA TCACAATCAC  
AGCTCTTGGC GCAGACTGTA TACCTATAGT CTTTGCAGAT CCTGTGAAAA  
AAGCATGTGG GGCTGCTCAC TCGGGCTGGA AGGGCACTTT GTTGGGCGTC  
GCTATGGCTA CTGTGAATGC TATGATAGCA

TABLE 25

10 SEQ ID NO. 24

GCAGATTTGG CATAAAAGTC TTTGGGGGAA AAAGGTGCCT GACTGAAGAA  
TGGCAGAAGC AGTCTTGATA GATCTCTCTG GTTTACAATT GAACTCTCAG  
GAAAACGTGC ATCAGATGGT ACTGAAGACG CAGGATGGTA TTCACGACCA  
CCATGCCCCC AAGGCCAAGT TCCTTTGTAT AATATGTTGC AGCGATGCCA  
15 CCAATGGAAG GGGTGGGGAA TATGGCCTCT GTGAACTGGA AGCAGGAAAT  
GGCAAAACAA GTCACGCGGA AAATTCGAGA CTGTTAGCCG T

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TABLE 26

SEQ ID NO. 25

TTTTTTTTTTT TTTTTTTTAA ACAAGGAAAC AAAACTAGCA CTCATCGCTT  
TTTAGACAAT ACATAATTAT TCAAAATTAA CTATTACCGG AAGGCAAGGG  
5 GGCCATACTA ATGGGCCTTG TCTCACATGA GTGCATGTGG GTAGGTGCAG  
GACGACTGAC ATTATGCAGA AACGAATTTT AATTTTAAAT CTTTAGTTTG  
ATTTAAACAT TGCTTTTAGT ATGATGACAA CACCAGCTGT GCAGAAAGGG  
CTCTGGAGAT GCGTTCATAG CAGCACACAC CTGCGGCTCT TCTTCGGTTC  
TGGAGGCT

10

TABLE 27

SEQ ID NO. 26

CTCACACCCC AGCTCGCGGC CGCCGAGGAG AGCGCGGGAA GCGCCCCGCG  
TGATTTGGCA TAAAAGTCTT TGGGGGAAAA AGGTGCCTGA CTGAAGAATG  
15 GCAGAAGCAG TCTTGATAGA TCTCTCTGGT TTACAATTGA ACTCTCAGGA  
AAACTGT CAT CAGATGGTAC TGAAGACGCT GGATGGTATT CACGACCACC  
ATGCCCCCAA GGCCAAGTTC CTTTGTATAA TATGTTGCAG CGATGCCACC  
AATGGAAAGG GTGGGGAATA TGGCCTCTGT GAACTGGAAG CAGGAATGGC

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## TABLE 28

SEQ ID NO. 27

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTACA GTACATACAC  
ACAGTATTTT ATTAGCCAT AATGAAATTA TCAAACCTAT AGGAAAAATT  
5 GATGGATCTG GAATTATTTA TTATGAGCAA AATAATCCAG ACTCAGAATA  
AGAAACACCA CATGTTCTTT CTTATATATA AATTCTAACC TTTAATGTTT  
ATGTAAACAT ACATGTATAT GGCTGTGTAA ATCTGTGGGT ATAAGTGTGG  
ATGGGTGTTG AAAC TAGAAA GGGAACATAA AAGGGGGATT GTGCAAGGGA  
GAACAAAACA CATGAGACAG GAAAGAGGGG CTTCTGCGGT

10

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SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Mary E. Russell  
Ulrike Utans

(ii) TITLE OF INVENTION: Mediators of Chronic Allograft  
Rejection

(iii) NUMBER OF SEQUENCES: 43

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fish & Richardson  
(B) STREET: 225 Franklin Street  
(C) CITY: Boston  
(D) STATE: Massachusetts  
(E) COUNTRY: U.S.A.  
(F) ZIP: 02110-2804

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
(B) COMPUTER: IBM PS/2 Model 50Z or 55SX  
(C) OPERATING SYSTEM: MS-DOS (Version 5.0)  
(D) SOFTWARE: WordPerfect (Version 5.1)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/171,385  
(B) FILING DATE: DEC-21-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Fraser, Janis K.  
(B) REGISTRATION NUMBER: 34,819  
(C) REFERENCE/DOCKET NUMBER: 05433/014001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 542-5070  
(B) TELEFAX: (617) 542-8906  
(C) TELEX: 200154

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCTGCTGTCA TTAGAAGGTC CTCGGTCCCA CCGTGTATA TCCACCTCCA ATTAGGGCAA 60



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TACAGAAATA GCTTTCTTGG CTGGGGGACC AGTTGGCTTC TGGTGTCTT TGTTTTTCTC 120  
 CTCACACATC AGAATCATTC TCAAGATGGC AGATCTCTTG CCCAGCATCA TTCTGAGAAA 180  
 GTCAGAGTAA CTGAACGTCT CCTCGGAGCC ACTGGACACC TCTCTAATTA ATTCTTCAG 240  
 CTCTAGATGG GTCTTGGGAA CCCAAGTTTC TCCAGCATTC GCTTCAAGGA CATAATATCG 300  
 ATATCTCCAT TGCCATTCAG ATCAACTCAT G 331

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ACGAGAATAT GGCTGTAATC TGGAGGACAT CATTGTTGTT CTGGGCCCTT CAGTGGGATC 60  
 TGCTGCTTTA CCTTCCAGAG AATCAGCAAC CTCATTACC AAGTCATCT GTGTGTGAGA 120  
 ACGTTGACT 129

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTTTTTTTTT TTGCAGCCAT TGTAAGGA TACGGGAAGC ATTTATCGAA AATCCAGAC 60  
 AAGAACCTCA TTCTCTAAGG GATATGAAGC CTATCTGTGT ACCGAAGTTA AGGCCATCAC 120  
 GGACATGGGA GAAAACTTC TCAGGATGGC AAGATGTGCA GAGGTCAAGA TCTTCCTCCT 180  
 GGTCTTGAAT ATCTGTGGAA GAATTCCTCC TGCTTCTAGA GATCCTGTGC TTTTCGGATG 240  
 TCAACGTAGG GATTGGTGA GTCAAACTGT CTCACACACG AAGGATGAAC ATTGTGAAAT 300  
 GAGGTTGCTG ATCTCTGG 318

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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GAGGAGCCAG CCAACACACT GCAGCCTCAT CGTCATCTCC CCACCTAAGG CCACCAGCGT 60  
 CTGAGGAGCT ATGAGCCAGA GCAAGGATTT GCAGGGAGGA AAAGCTTTTG CACTGCTGAA 120  
 AGCCCAGCAG GAAGAGAGGT TGGATGGGAT CAACAAGCAC TTCCTCGATG ATCCCAAGTA 180  
 CAGCAGTGAT GAGGATCTGC AGTCCAAACT GGAGGCCTTC AAGACGAAGT ACATGGAGTT 240  
 TGATCTGAAT GGCAATGGAG ATATCGATAT TATGTCCTTG AAGCGAATGC TGGAGAAACT 300  
 TGGGGTTCCC AAGACCCATC TAGAGCTGAA GAAATTAATT AGAGAGGTGT CCACTGGGCTC 360  
 CGAGGAGACG TTCAGTTACT CTGACTTTCT CAGAATGATG CTGGGCAAGA GATCTGCCAT 420  
 CTTGAGAATG ATTCTGATGT ATGAGGAGAA AAACAAAGAA CACCAGAAGC CAACTGGTCC 480  
 CCCAGCCAAG AAAGCTATT CTGAGTTGCC CTAATTGGAG GTGGATATAA CACGGTGGGA 540  
 CCGAGGACCT TCTAATGACA GCAGCATGGG AAAAGAAGAA GCAGTTGTGA GCCAGAGTCA 600  
 AACTAAATAA ATAATGCTCC CTAGTGC 627

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Ser Gln Ser Lys Asp Leu Gln Gly Gly Lys Ala Phe Gly Leu Leu Lys  
 1 5 10 15  
 Ala Gln Gln Glu Glu Arg Leu Asp Gly Ile Asn Lys His Phe Leu Asp Asp  
 20 25 30  
 Pro Lys Tyr Ser Ser Asp Glu Asp Leu Gln Ser Lys Leu Glu Ala Phe Lys  
 35 40 45 50  
 Thr Lys Tyr Met Glu Phe Asp Leu Asn Gly Asn Gly Asp Ile Asp Ile Met  
 55 60 65  
 Ser Leu Lys Arg Met Leu Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu  
 70 75 80 85  
 Leu Lys Lys Leu Ile Arg Glu Val Ser Ser Gly Ser Glu Glu Thr Phe Ser  
 90 95 100  
 Tyr Ser Asp Phe Leu Arg Met Met Leu Gly Lys Arg Ser Ala Ile Leu Arg  
 105 110 115  
 Met Ile Leu Met Tyr Glu Glu Lys Asn Lys Glu His Gln Lys Pro Thr Gly  
 120 125 130 135  
 Pro Pro Ala Lys Lys Ala Ile Ser Glu Leu Pro  
 140 145

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## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	18
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CACATCTTGC CATCCTGA

18

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 7:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	18
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CATGGTGCTT GAGAACAG

18

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 8:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	310
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GTTTAATGCA GAGAAATTTT ACCGAATAAA GACTGATCAC GCCAGGTAAG TATGGGTAAT 60  
GGGGAAGAAG GAGCCTGAAT CTTACGATGG AATAATTACA AATCAGAGAG GAATCACAAT 120  
CACAGCTCTT GCGCGAGACT GTATACCTAT AGTCTTTGCA GATCCTGTGA AAAAAGCATG 180  
TGGGGCTGCT CACTCGGGCT GGAAGGGCAC TTTGTTGGGC GTCGCTATGG CTACTGTGAA 240  
TGCTATGATA GCAGAATATG GCTGTAATCT GGAGGACATC ATTGTTGTTT TGGGCCCTTC 300  
AGTGGGATCT 310

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 9:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	274
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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TTTTTTTTTC TTATATATAA ATTCTAACCT TTAATGTTTA TGTAACATA CATGTATATG 60  
GCTATGTAAA TCTGTGGGTA TAAGTGTGGA TAGGTGTTGA AACTAGAAAG GGAACATAAA 120  
AGGGGATTGT GCAAGGGAGA ACAAACACA TGAGACAGGA AAGAGGGGCT TCTGCAGTGA 180  
AAGGGTACAC AAGGGGCCAG GGAAAGGGAG AGCGAGGGCC AGAAAAACAT GGTGCTTGAG 240  
AACAGCATAA GGAACCTGTA TTTATAAGGC AGTT 274

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	388
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CCGAGTCTCG CGTCTACCAG AGCTGCAAGA TGTCTGTGCT CCCTGGAATA ATTGTCCTTG 60  
TGGGACGATC CTCATGTGCC TGGTGTGCCT GCTTGCTAGT AGGAGGAATA ATACCGGTTT 120  
ATTCTCCTAC CGGAACACCA ATATGTATAT GTGCATCGGC CCAAGTCAT CATTGAAAAC 180  
ACAGTGTCT CAAGTGGACA AGACCTTCAC TGGATTGTTT AAGAGAGATC CAGCCTTACA 240  
AGAAGGAAAA CTAGAGACCA AATAAATCC TCTTCCTTCT CGATGGGTAT CATCTGCTTC 300  
TTCTTCCTAA AAGACTGGGG GAGCIATCTC TCATAGTGAG TACATTCAGT GTGCAAGTGG 360  
CTCTCAGAGT AGACTCAGTC CTTGCTTG 388

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## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 11:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	362
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
TCGAGTTTT TTTTTTTTT TTTATATATA AATTCTAACC TTTAATGTTT ATGTAAACAT   60
ACATGTATAT GGCAATGTAA ATCTGTGGGT ATAAGTGTGG ATAGGTGTTG AAAC TAGAAA   120
GGGAACATAA AAGGGGATTG TGCAAGGGAG AACAAACAC ATGACAGGAA AGAGGGGCTT   180
CTGCAGTGAA AGGGTACACA AGGGGCCAGG GAAAGGGAGA GCGGAGGGCC AGAAAAACAT   240
GGTGCTTGAG AACAGCATAA GGAAACCTGT ATTTTATAAG GCAGTTAAAA TATACATTTA   300
AAAGGAACG                                     309
```

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	362
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
TTTTTTTTTT TTTTTTTTT TTTTTTTTT CTTATATATA AATTCTAACC TTTAATGTTT   60
ATGTAAACAT ACATGTATAT GGCTATGTAA ATCTGTGGGT ATAAGTGTGG ATAGGTGTTG   120
AAAC TAGAAA GGAACATAA AAGGGGATTG TGCAAGGGAG AACAAACAC ATGAGACAGG   180
AAAGAGGGGC TTCTGCAGTG AAAGGGTACA CAAGGGGCCA GGGAAAGGGA GACGGAGGGC   240
CAGAAAAACA TGGTGCTTGA GAACAGCATA AGGAAACCTG GTATTTTATA AGGCAGTTAA   300
AAATATACAT TTAAAGGAA ACGTTATCT CCCCTACTGC ATTTGATTCA AATGAGAAGG   360
TG                                     362
```

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	347
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```
GAAAAAGGTG CTGACTGAA GAATGGCAGA AGCAGTCTTG ATAGATCTCT CTGGTTTACA   60
```

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ATTGAACTCT CAGGAAACT GTCATCAGAT GGTACTGAAG ACGCTGGATG GTATTCACGA 120  
 CCACCATGCC CCCAAGGCCA AGTTCCTTTG TATAATATGT TGCAGCGATG CCACCAATGG 180  
 AAAGGGTGGG GAATATGGCC TCTGTGAACT GGAAGCAGGA AATGGCTTTT CAAGTCTCGC 240  
 GGGAAAATTC GAGACTGTTA GCCATCCAGC CTGGCTGCCT CTTTGTATTC AGTTAAACAA 300  
 AAATAGATGA GGAGGATCTG AGCCGCGTTA AGGTGATTGT GCCCGAG 347

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT ACATACACAC AGTATTTTAT 60  
 TTAGCCATAA TGAAATTATC AAACCTATAG GAAAATTGA TGGATCTGGA ATTATTTTAT 120  
 ATGAGCAAAA TAATCCAGAC TCAGAATAAG AACACCACA TGTTCTTTCT TATATATAAA 180  
 TTCTAACCTT TAATGTTTAT GTAAACATAC ATGTATATGG CTATGTAAAT CTGTGGGTAT 240  
 AAGTGTGGAT AGGTGTTGAA ACTAGAAAGG GAACATAAAA GGGGATTGTG CAAGGGAGAA 300  
 CAAAACATAT GAGACAGGAA AGAGGGGCTT CTGTAGTGAA AGGGTACCAA 350

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCTCAGCTCA CTCAATCTTT TCAGTAGTTC CAAACGGAGA GATCCCAAAG TGGTTGTTCA 60  
 AGAAAACCTC CGCGGCCTGG CAAATGCTGC AGGGTTTAAT GCAGAGAAAT TTTACCGAAT 120  
 AAAGACTGAT CACGCCAGGT AAGTATGGGT AATGGGGAAG AAGGAGCCTG AATCTTACGA 180  
 TCGAATAATT ACAAATCAGA GAGGAATCAC AATCACAGCT CTTGGCAGAC TGTATACCTA 240  
 TAGTCTTTGC ACATCCTGTG AAAAAAGCAT GTGGGGCTGC TCACTCGGGC TGAAGGGCA 300  
 CTTTGTGGG CGT 313

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 16:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 295  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```
TTTTTTTTTT TTTTTTTTTT TTCTTATATA TAAATCTCTAA CCTTAAATGT TTATGTAAAC   60
ATACATGTAT ATGGCTATGT AAATCTGTGG GTATAAGTGT GGATAGGTGT TGAAACTAGA   120
AAGGGAACAT AAAAGGGGAT TGTGCAAGGG AGAACAAAAC ACATGAGACA GGAAAGAGGG   180
GCTTCTGCAG TGAAAGGGTA CACAAGGGGC CAGGGAAAGG GAGAGCGGAG GGCCAGAAAA   240
ACATCGTGCT TGAGAAATAGC ATAAGGAAAC CTGGTATTTA TAAGGCAGTT AAAAA      295
```

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 17:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```
TCGGGCAGGA AGGGCACTTT GTTGGGCGTC GCTATGGCTA CTGTGAATGC AGTGATAGCA   60
GAATATGGCT GTAGTCTGGA GGACATCGTT GTTGTCTGCG GCCCTTCAGT GGGATCTTGC   120
TGCTTTACTC TTCCCAGAGA ATCAGCAACC TCATTTTACA ATGTTTCATCC TTCGTGTGTG   180
AGACAGTTTG ACTCACCAA TCCCTGCGTT GACATCCGAA AAGCCACCAG GATTCCTTCTA   240
GAACGAGGAG GAATTCTTCC ACAGAATATC AAGACCAGGA GGAAGATCTG ACCTCTGCAC   300
ATCTGCCATC TGAGAG                                     316
```

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 18:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```
TTTTTTTTTT TTTTTTTTATA TATAAATTCT AACCATTCTAA TGTTTACGTA AACATACATG   60
TATATGGCTA TGTAATCTG TGGGTATAAG TGTGGATAGG AGTTGAAACT AGAAAGGGAA   120
CATAAAAGGG GATTGTGCAA GCGAGAACAA AACACATGAG ACAGGAAAGA GGGGCTTCTG   180
CAGTGAAAGG GTACACAAGG GCGCAGGGAA AGGGAGAGCG GAGGGCCAGA AAAACATGGT   240
GCTTGAGAAC AGCATAAGGA AACCTGGTAT TTTATAAGGC AGTTAAAAAT ATACATTCTA   300
```

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AAGGAAACGT TTATCTCCCC

320

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	317
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

CCGGGGCGCC GGCCGGCCGT GCGGGAACA CCCGAATCC GGTGCCCGGA GGCCCGGACG      60
CTGTGAGGCG GCGGAGCGGG CGGACCCGTT CGGGCGACTC TGGGGTTCGT TCCCCGAGGC    120
TGCAGCTCAC ACCCCAGCTC GCGGCCGCCG AGGAGAGCGC GGGAAGCGCC CCGCGTGATT    180
TGGCATAAAA GTCTTTGGGG GAAAAGGTG CCTGACTGAA GAATGGCAGA AGCAGTCTTG      240
ATAGATCTCT CTGGTTTACA ATTGAACTCT CAGGAAACT GTCATCAGAT GGTACTGAAG      300
ACGCTGGATG GTATCAC                                     317

```

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 20:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	345
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

TTTTTTTTTT TTTTTTTTTT ACAGTACATA CACACAGCAT TTTATTTAGC CATAATGAAA      60
TTATCAAACT TATAGGAAAA ATTGATGGAT CTGGAATTAT TTATTATGAG CAAAATAATC    120
CAGTCTCAGA ATAAGAAACA CCACATGTTT TTTCTTATAT ATAAATTCTA ACCTTTAATG    180
TTTATGTAAA CATACAGTAT ATGGCTATGT AAATCAGTGG GTATAAGTGT GGATAGGTGT    240
TGAAACTAGA AAGGGAACAT AAAAGGGGAT TATCGAAGGG AGAACAAAAC ACATGAGACA    300
GGAAAGAGGG GCAATAGTAG TGAAAGGGAA TATAAGGGGC CAGGG                      345

```

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 21:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	329
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:



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CCTCCGCAGC TGGCAAATGC TGCAGGGTTT AATGCAGAGA AATTTTGCCG AATAAAGACT 60  
GATCAGGCCA GGTAAGTATG GGTAATGGGG AAGAAGGAGC CTGAATCTTA GCATGGAATA 120  
ATTACAAATC AGAGAGGAAT CACAATCACA GCTCTTGGCG CAGACTGTAT ACCTATAGTC 180  
TTTGCAATC CTGTGAAAAA AGCATGTGGG GCTGCTCACT CGGGCTGGAA GGGCACTTTG 240  
TTGGGCGTCG CTATGGCTAC TGTGAATGCT ATGATAGCAG AATATGGCTG TAATCTGGAG 300  
GACATCATTG TTGTTCTGGG CCCTTCAGT 329

(2) INFORMATION FOR 'SEQUENCE IDENTIFICATION NUMBER: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	321
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTTTTTTTTT TTTTTTTTTT TACAGTACAT ACACACAGTA TTTTATTTAG CCATAATGAA 60  
ATTATCAAAC TTATAGGAAA AATTGATGGA TCTGGAATTA TTTATTATGA GCAAATAAT 120  
CCAGACTCAG AATAAGAAAC ACCACATGTT CTTTACTTAT ATATAAATTC TAACCTTTAA 180  
TGTTTATGTA AACATACATG TATATGGCTA TGTAATCTG TGGGTATAAG TGTGGATAGG 240  
TGTTGAAACT AGAAAGGGAA CATAAACCGG GGATTATGCA AGGGAGAACA AAACACATGA 300  
GACAGGAAAG AGGGGCTTCT G 321

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## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 23:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	280
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

CCTCCGCAGG CTGGCAAATG CTGCAGGGTT TGGTGTAGAG AAATTTTACC GAATAAAGAC   60
TGATCATGTT AGTGAAGTAT GGGTAATGGG GAAGAAGGAG CCTGAATCTT ACGATGGAAT   120
AATTACAAAT CAGAGAGGAA TCACAATCAC AGCTCTTGGC GCAGACTGTA TACCTATAGT   180
CTTTGCAGAT CCTGTGAAA AAGCATGTGG GGCTGCTCAC TCGGGCTGGA AGGGCACTTT   240
GTTGGGCGTC GCTATGGCTA CTGTGAATGC TATGATAGCA                          280

```

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 24:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	291
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

GCAGATTTGG CATAAAAGTC TTTGGGGGAA AAAGGTGCCT GACTGAAGAA TGGCAGAAGC   60
AGTCTTGATA GATCTCTCTG GTTACAATT GAACTCTCAG GAAACTGTC ATCAGATGGT   120
ACTGAAGACG CAGGATGGTA TTCACGACCA CCATGCCCCC AAGGCCAAGT TCCTTTGTAT   180
AATATGTTGC AGCGATGCCA CCAATGGAAA GGGTGGGGAA TATGGCCTCT GTGAACTGGA   240
AGCAGGAAAT GGCAAAACAA GTCACGCGGA AAATTCGAGA CTGTTAGCCG T          291

```

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 25:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	307
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

TTTTTTTTTT TTTTTTTTAA ACAAGGAAAC AAAACTAGCA CTCATCGCTT TTTAGACAAT   60
ACATAATTAT TCAAAATTAA CTATTACCGG AAGGCAAGGG GGCCATACTA ATGGGCCTTG   120
TCTCATGTA GTGCATGTGG GTAGGTGCAG GACGACTGAC ATTATGCAGA AACGAATTTT   180
AATTTTAAAT CTTTAGTTTG ATTTAAACAT TGCTTTTAGT ATGATGACAA CACCAGCTGT   240

```

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GCAGAAAGGG CTCTGGAGAT GCGTTCATAG CAGCACACAC CTGCGGCTCT TCTTCGGTTC 300  
 TGGAGGCT 307

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	300
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CTCACACCCC AGCTCGCGGC CGCCGAGGAG AGCGCGGGAA GCGCCCCGCG TGATTGGCA 60  
 TAAAAGTCTT TGGGGGAAAA AGGTGCCTGA CTGAAGAATG GCAGAAGCAG TCTTGATAGA 120  
 TCTCTCTGGT TTACAATTGA ACTCTCAGGA AAAGTGTCTAT CAGATGGTAC TGAAGACGCT 180  
 GGATGGTATT CACGACCACC ATGCCCCCAA GGCCAAGTTC CTTTGTATAA TATGTTGCAG 240  
 CGATGCCACC AATGGAAAGG GTGGGGAATA TGGCCTCTGT GAACTGGAAG CAGGAATGGC 300

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	340
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTACA GTACATACAC ACAGTATTTT 60  
 ATTTAGCCAT AATGAAATTA TCAAACTTAT AGGAAAATT GATGGATCTG GAATTATTTA 120  
 TTATGAGCAA AATAATCCAG ACTCAGAATA AGAAACACCA CATGTTCTTT CTTATATATA 180  
 AATTCTAACC TTTAATGTTT ATGTAAACAT ACATGTATAT GGCTGTGTAA ATCTGTGGGT 240  
 ATAAGTGTGG ATGGGTGTTG AAAGTAGAAA GGGAACATAA AAGGGGGATT GTGCAAGGGA 300  
 GAACAAAACA CATGAGACAG GAAAGAGCGG CTTCTGCGGT 340

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## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 28:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	10
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

AGCCAGCGAA 10

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 29:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	10
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

AATCGGGCTG 10

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 30:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	10
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

TCTGTGCTGG 10

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 31:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	18
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

CCTAGAAACC CTGAGAAC 18

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## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 32:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	18
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

GAGTGCCGCT TATTGTAG 18

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 33:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	26
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

GTCAATTCGC TATGAGCCAG AGCAAG 26

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 34:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	27
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

GAAGAAGCAG TTGTGAGCGT CGACCAA 27

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 35:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	24
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

ATCCCAAGTA CAGCAGTGAT GAGG 24

## (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 36:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	24
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

GTCCCCCAGC CAAGAAAGCT ATTT 24

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	23
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

CTCGCGCTAC TCTCTCTTTC TGG 23

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	25
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

TTAAGTGCGA TCGAGACATG TAAGC 25

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	19
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

TGAGAAAGTC AGGCTAGCT 19

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	18
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

ACCTCTACCA GCATCTGC 18

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 41:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 21  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

TGAAGGGAAA AGGGATGATG G 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

Glu Val Ser Ser Gly Ser Gly Glu Thr Phe Ser Tyr Pro Asp Phe Leu  
 1 5 10 15  
 Arg Met Met Leu Gly Lys Arg Ser Ala Ile Leu Lys Met Ile Leu Met  
 20 25 30  
 Tyr Glu Glu Lys Ala Arg Glu Lys Glu Lys Pro Thr Gly Pro Pro Ala  
 35 40 45  
 Lys Lys Ala Ile Ser Glu Leu Pro  
 50 55

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

ACCTCTACCA GCATCTGCTG AGCTATGAGC CAAACCAGGG ATTTACAGGG AGGAAAAGCT 60  
 TTCGGACTGC TGAAGGCCCA GCAGGAAGAG AGGCTGGATG AGATCAACAA GCAATTCCTA 120  
 GACGATCCCA AATATAGCAG TGATGAGGAT CTGCCCTCCA AACTGGAAGG CTCAAAGAG 180  
 AAATACATGG AGTTTGACCT TAATGGAAAT GGCGATATTG ATATCATGTC CCTGAAACGA 240  
 ATGCTGGAGA AACTTGGAGT CCCCAAGACT CACCTAGAGC TAAAGAAATT AATTGGAGAG 300  
 GTGTCCAGTG GCTCCGGGGA GACGTTTCAGC TACCCTGACT TTCTCAGGAT GATGCTGGGC 360  
 AAGAGATCTG CCATCCTAAA AATGATCCTG ATGTATGAGG AAAAAGCGAG AGAAAAGGAA 420  
 AAGCCAACAG GCCCCCCAGC CAAGAAAGCT ATCTCTGAGT TGCCCTGATT TGAAGGGAAA 480  
 AGGGATGATG G 491

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What is claimed is:



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Claims:

1. A method of identifying a gene which is differentially expressed in an allograft of a given tissue type compared to a syngraft of said tissue type, comprising
  - obtaining mRNA from said allograft and from said syngraft; and
  - determining whether the amount per cell of a given gene transcript from said allograft is increased or decreased compared to the amount per cell from said syngraft.
2. A method of diagnosing allograft rejection in a patient, comprising detecting a differentially expressed allograft gene transcript or polypeptide product thereof in an allograft tissue, wherein detection of said differentially expressed allograft gene transcript or polypeptide product is an indication that said allograft tissue is undergoing transplant rejection.
3. The method of claim 2, wherein said differentially expressed allograft gene encodes allograft inflammatory factor-1 (AIF-1) or allograft inflammatory factor-2 (AIF-2).
4. An isolated DNA encoding AIF-1.
5. The isolated DNA of claim 4, wherein said AIF-1 is human AIF-1 (SEQ ID NO:42).
6. The isolated DNA of claim 5, wherein said DNA comprises the sequence of SEQ ID NO:43.
7. An isolated DNA comprising a sequence encoding an immunogenic fragment of human AIF-1 (SEQ ID NO:42).

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8. An isolated DNA which hybridizes at high stringency to a 20 nucleotide fragment of SEQ ID NO:1, 4, or 43.

9. A substantially pure preparation of AIF-1 polypeptide.

10. The preparation of claim 9, wherein said polypeptide is human AIF-1 (SEQ ID NO:42) or rat AIF-1 (SEQ ID NO:5).

11. An isolated DNA comprising the sequence of SEQ ID NO:2, 3, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27.

12. An isolated DNA which hybridizes at high stringency to SEQ ID NO:2, 3, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27, said DNA encoding a naturally-occurring polypeptide or an antigenic fragment thereof.

13. A substantially pure preparation of AIF-2 polypeptide.

14. The method of claim 2, wherein said allograft gene encodes ubiquitin or P1.

15. The method of claim 2, wherein said allograft gene encodes galactose/N-acetyl-galactosamine macrophage lectin.

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16. A method of diagnosing allograft rejection comprising measuring the amount of a given differentially expressed allograft gene transcript or polypeptide product thereof in a sample of an allograft of a given tissue type, wherein an increase in said amount compared to the amount of said transcript or polypeptide product in a sample of normal tissue of said tissue type is an indication that said allograft is undergoing rejection.

17. A method of inhibiting rejection of a transplanted tissue in an animal, comprising introducing into said animal a compound which inhibits expression of a differentially expressed allograft gene that is upregulated during rejection of an allograft.

18. A method of inhibiting rejection of a transplanted tissue in an animal, comprising introducing into said animal a compound which inhibits binding of a cell-associated lectin to a carbohydrate ligand on said transplanted tissue.

19. The method of claim 18, wherein said lectin is galactose/N-acetyl-galactosamine macrophage lectin.

20. The method of claim 18, wherein said compound is a galactose/N-acetyl-galactosamine macrophage lectin-specific antibody.

21. The method of claim 18, wherein said compound comprises a carbohydrate-binding fragment of galactose/N-acetyl-galactosamine macrophage lectin.

22. A method of identifying a candidate compound capable of inhibiting allograft rejection, comprising

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(a) in an *in vitro* assay, contacting galactose/N-acetyl-galactosamine macrophage lectin with a carbohydrate ligand to which said lectin binds, in the presence of said candidate compound; and

(b) measuring binding of said lectin to said carbohydrate ligand, wherein a decrease in said binding in the presence of said candidate compound compared to said binding in the absence of said candidate compound is an indication that said candidate compound inhibits allograft rejection.

23. A method of identifying a candidate compound capable of inhibiting allograft rejection comprising

(a) contacting galactose/N-acetyl-galactosamine macrophage lectin with a carbohydrate ligand to which said lectin binds in the presence of said candidate compound, said contacting step being carried out *in vivo*; and

(b) measuring binding of said lectin to said carbohydrate ligand, wherein a decrease in binding in the presence of said candidate compound compared to binding in the absence of said candidate compound is an indication that said candidate compound inhibits allograft rejection.

24. An inhibitor of allograft rejection, comprising a soluble, carbohydrate-binding fragment of galactose/N-acetyl-galactosamine macrophage lectin in a pharmaceutical excipient.

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25. A method of diagnosing inflammation in a patient's blood vessel, comprising detecting a differentially expressed allograft gene transcript or polypeptide product thereof in said blood vessel, wherein detection of said differentially expressed allograft gene transcript or polypeptide product is an indication that said blood vessel is inflamed.

26. A method of inhibiting atherosclerosis in an animal, comprising introducing into said animal a compound which inhibits expression of a differentially expressed allograft gene that is upregulated during inflammation of blood vessels.

Fig. 1A

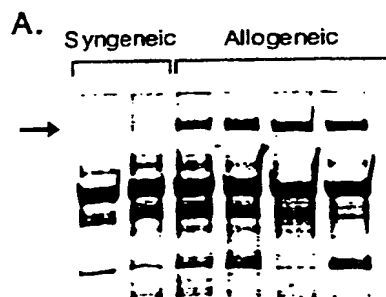
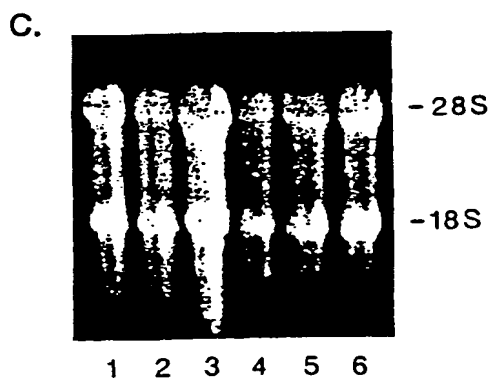


Fig. 1B



Fig. 1C



*Northern Analysis*

Fig. 2A

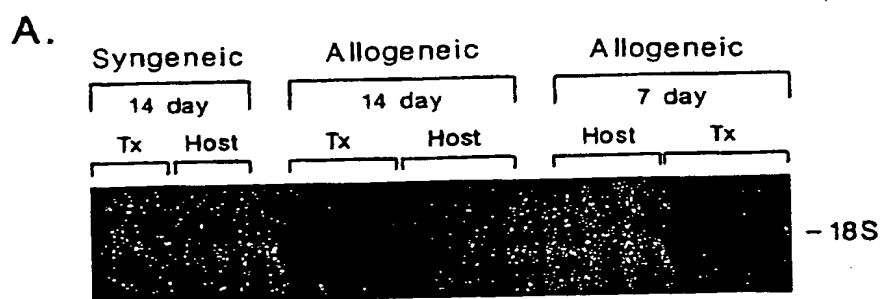
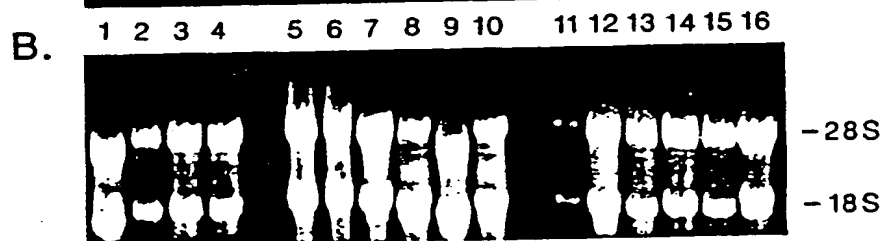


Fig. 2B



**Northern Analysis**

Tx (0 day)  
 Spleen (Host)  
 Spleen (LPS)  
 Liver  
 Lung  
 Kidney  
 Adrenal Gland  
 Ovary  
 Testis  
 Skeletal Muscle

A.

18S -



Fig. 3A

1 2 3 4 5 6 7 8 9 10 11 12

B.

28S -

18S -

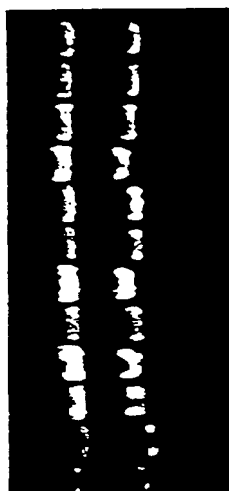


Fig. 3B



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Fig. 4A

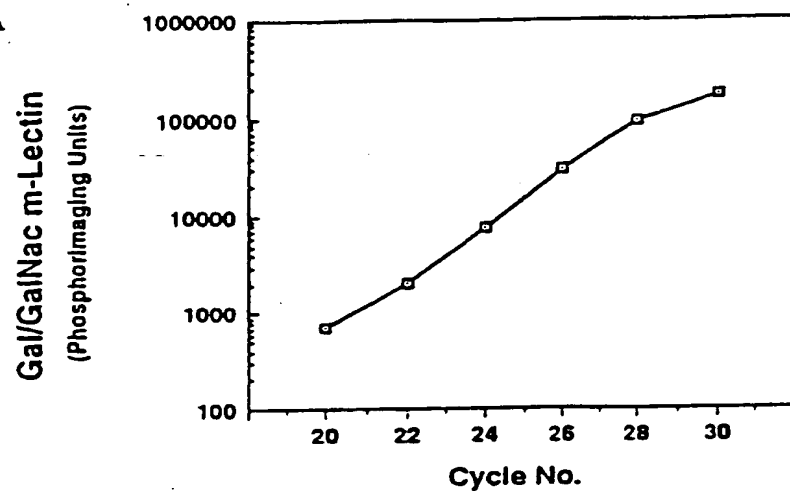
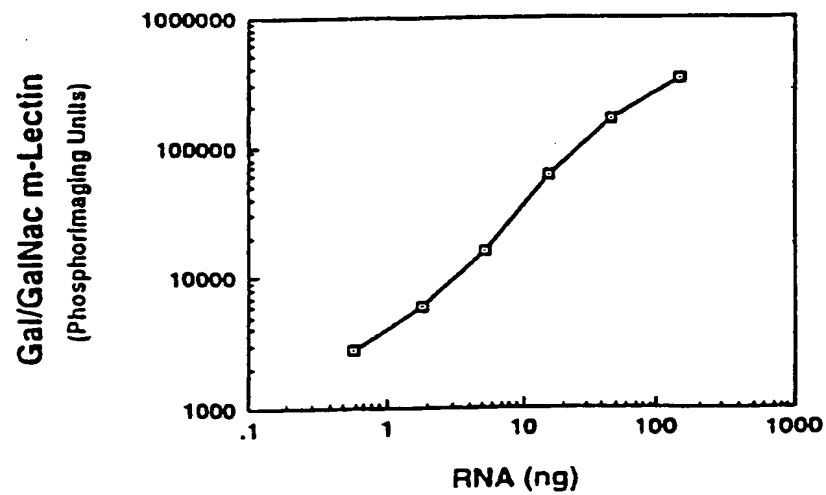


Fig. 4B



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Fig. 5

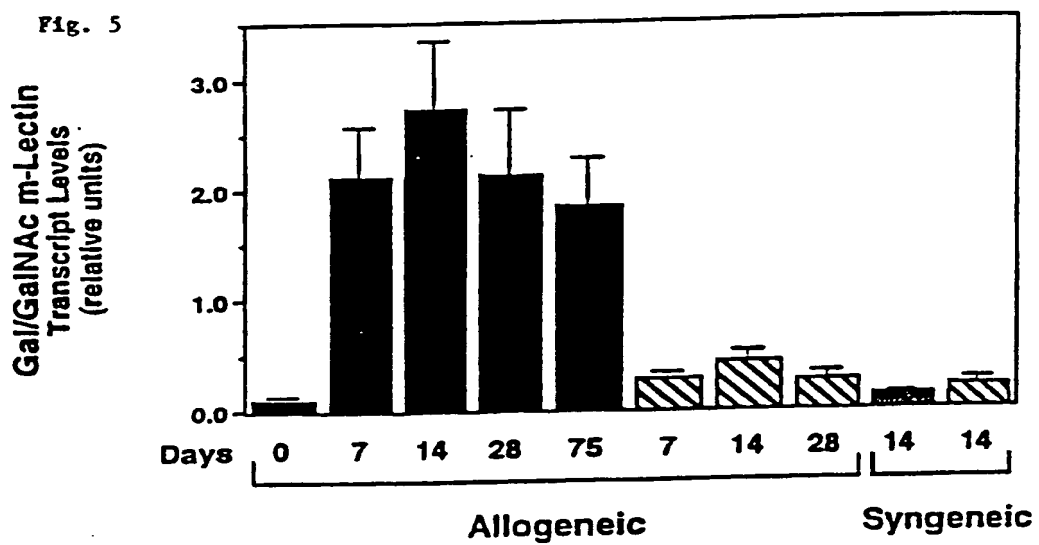
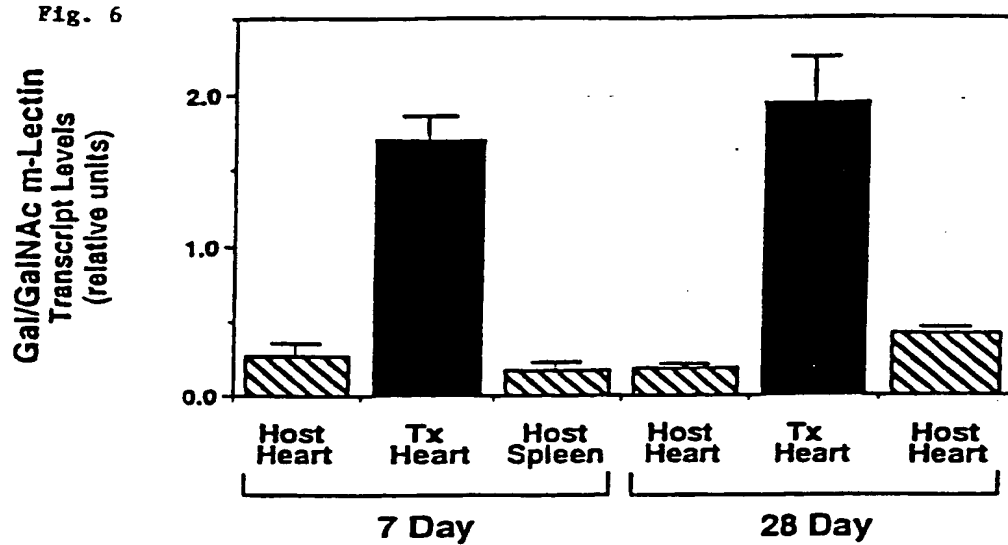


Fig. 6



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Fig. 7

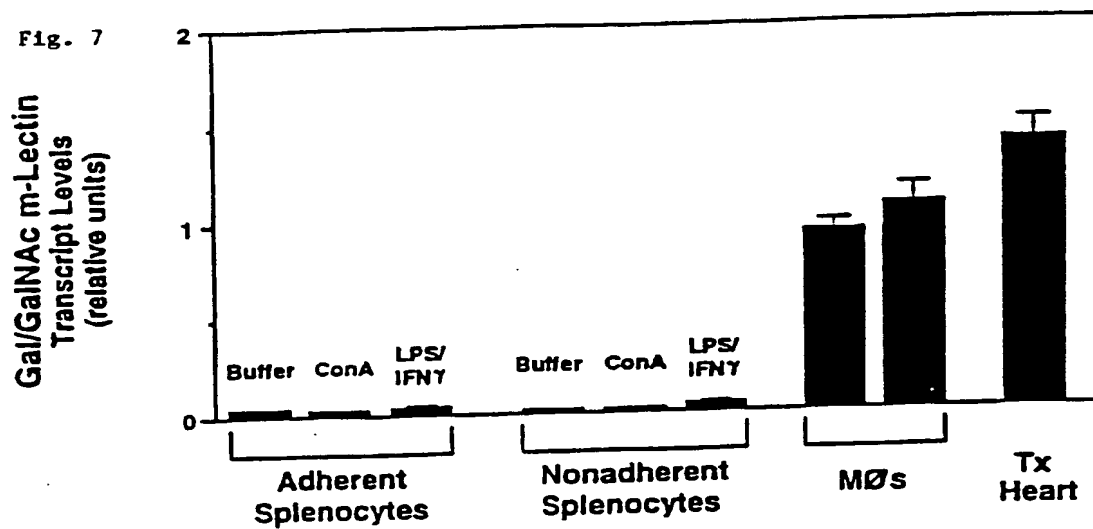




Fig. 8A

Fig. 8B

Fig. 8C

Fig. 8D

# *Differential mRNA Display*

Fig. 9A

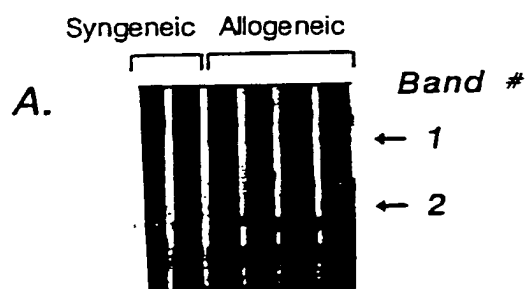
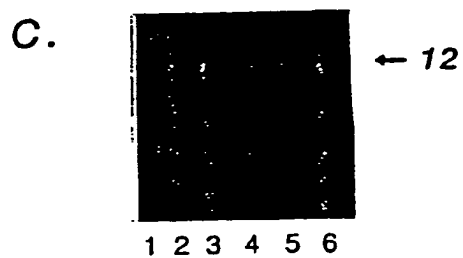


Fig. 9B



Fig. 9C



## Northern Analysis of Differential Display cDNAs

Fig. 10A

## A. PCR Fragment

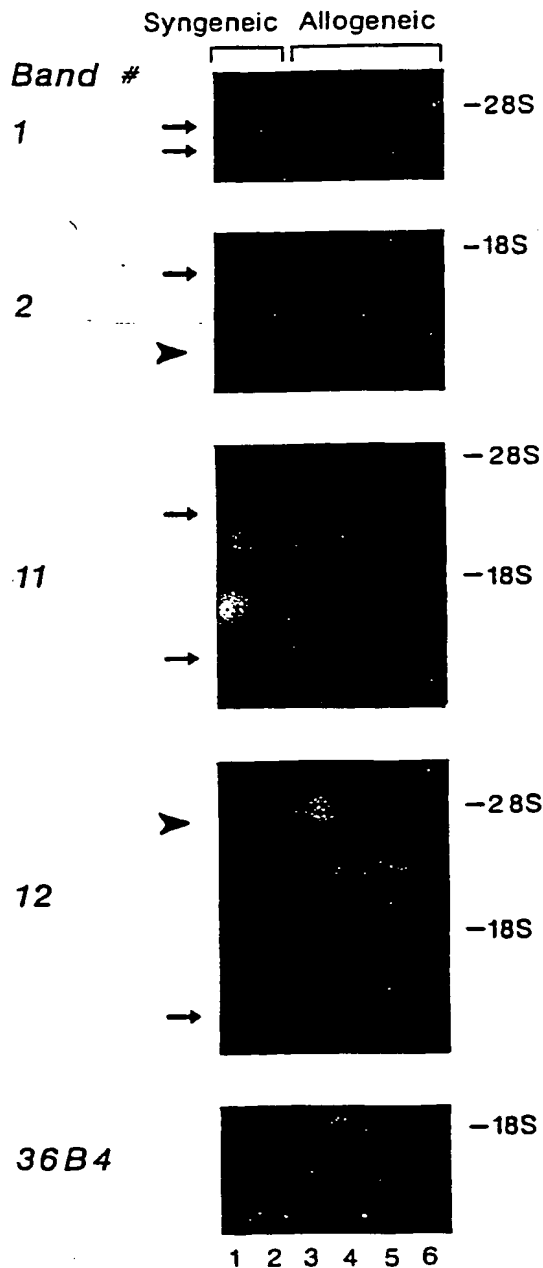
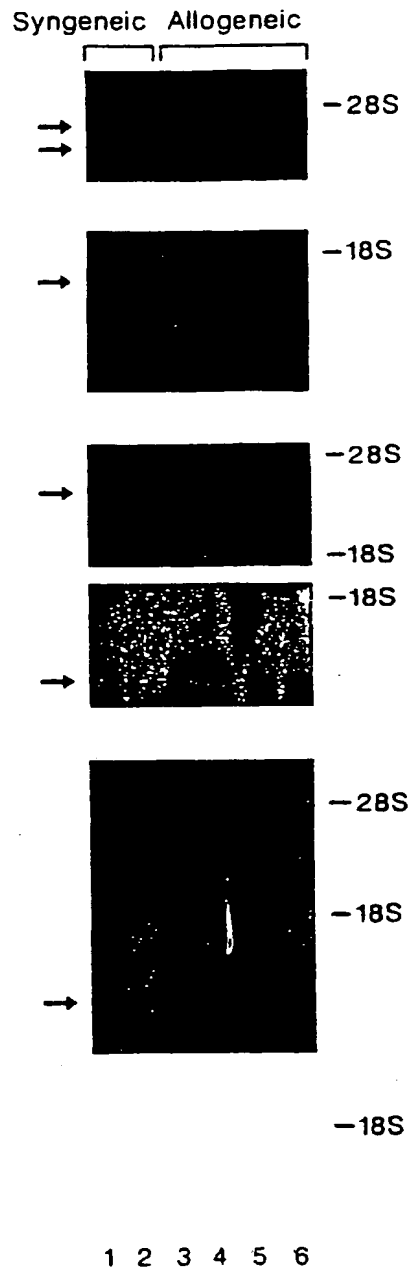


Fig. 10B

## B. Cloned Fragment



**A**

GAGGAGCCAGCCAACACACTGCAGCCTCATCGTCATCTCCCCACCTAAGGCCACCAGCGT 60  
CTGAGGAGCTATGAGCCAGAGCAAGGATTTGCAGGGAGGAAAAGCTTTTGGACTGCTGAA 120  
M S Q S K D L Q G G K A F G L L K  
AGCCCAGCAGGAAGAGAGGTTGGATGGGATCAACAAGCACTTCCTCGATGATCCCAAGTA 180  
18 A Q Q E E R L D G I N K H F L D D P K Y  
CAGCAGTGATGAGGATCTGCAGTCCAAACTGGAGGCCTTCAAGACGAAGTACATGGAGTT 240  
38 S S D E D L Q S K L E A F K T K Y M E F  
TGATCTGAATGGCAATGGAGATATCGATATTATGTCCTTGAAGCGAATGCTGGAGAAACT 300  
58 D L N G N G D I D I M S L K R M L E K L  
TGGGGTTCCCAAGACCCATCTAGAGCTGAAGAAATTAATTAGAGAGGTGTCCAGTGGCTC 360  
78 G V P K T H L E L K K L I R E V S S G S  
CGAGGAGACGTTTCACTTACTCTGACTTTCTCAGAATGATGCTGGGCAAGAGATCTGCCAT 420  
98 E E T F S Y S D F L R M M L G K R S A I  
CTTGAGAATGATTCTGATGTATGAGGAGAAAAACAAAGAACCAGAAAGCCAACTGGTCC 480  
118 L R M I L M Y E E K N K E H Q K P T G P - -  
CCCAGCCAAGAAAGCTATTTCTGAGTTGCCCTAATTGGAGGTGGATATAACACGGTGGGA 540  
138 P A K K A I S E L P  
CCGAGGACCTTCTAATGACAGCAGCATGGGAAAAGAAGAAGCAGTTGTGAGCCAGAGTCA 600  
AACTAAATAAATAATGCTCCCTAGTGC

SEQ ID NO: 4

FIG. 11A



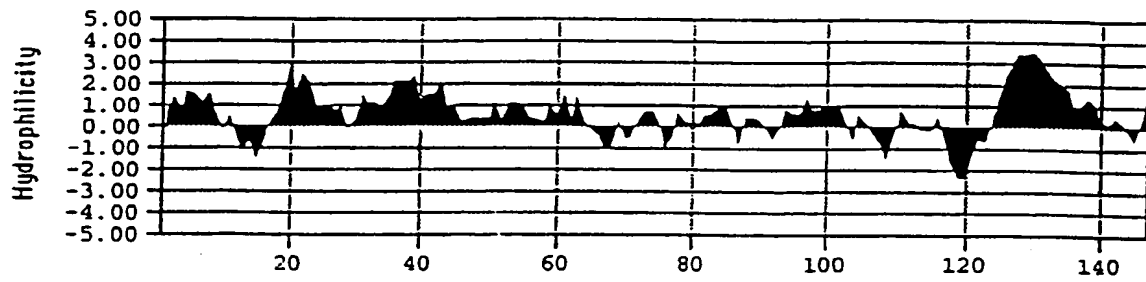
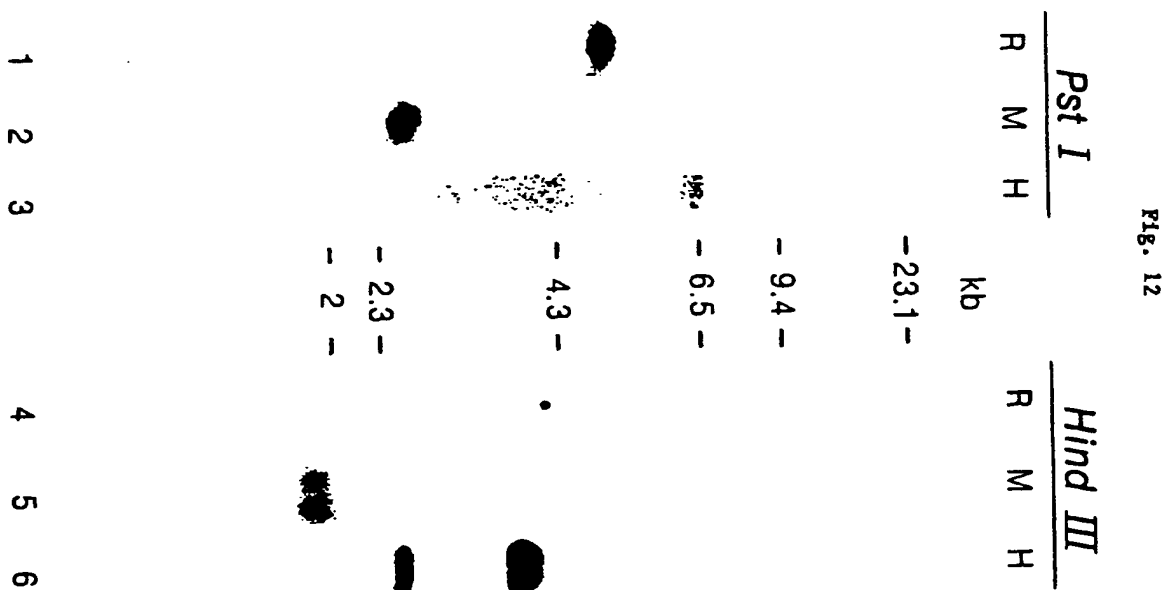
**B**

FIG. 11B



# Northern Analysis

Fig. 13A

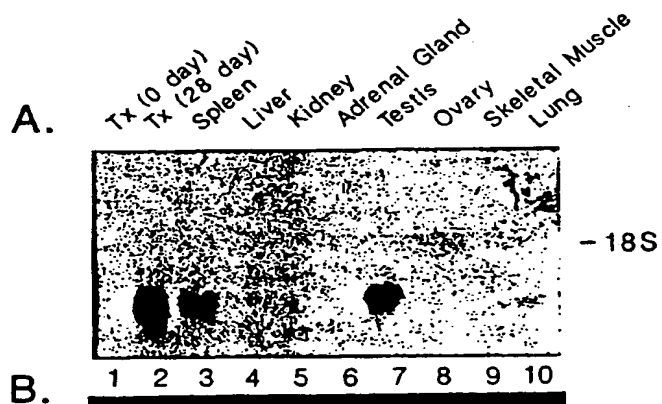
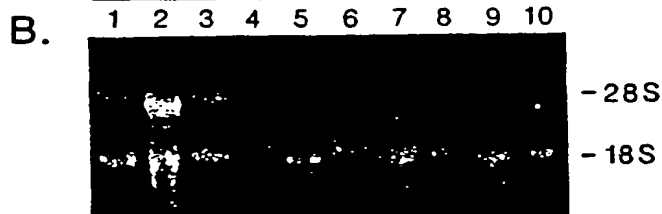


Fig. 13B



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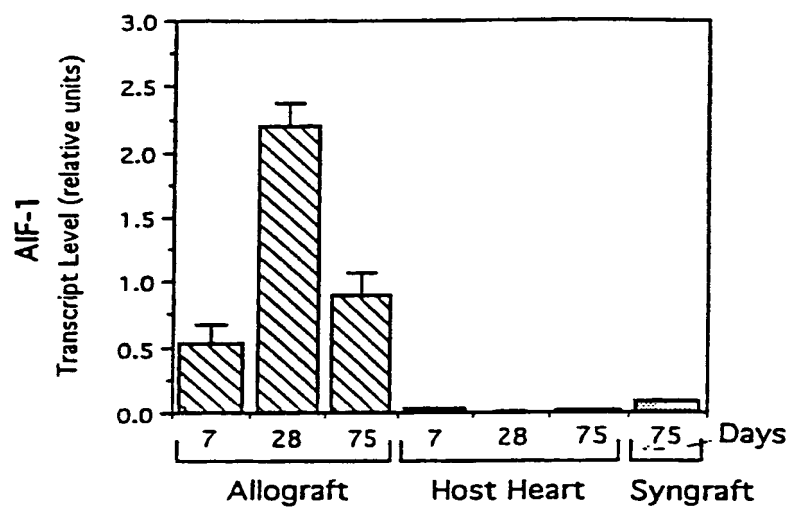


FIG. 14

Fig. 15A



Fig. 15B



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Fig. 16A

A.  
18s -  
TxH (0 day)  
TxH (28 day)  
Spleen  
Bone Marrow  
BM mφ  
ip BCG mφ  
ip PMN  
T cells  
SMC

Fig. 16B

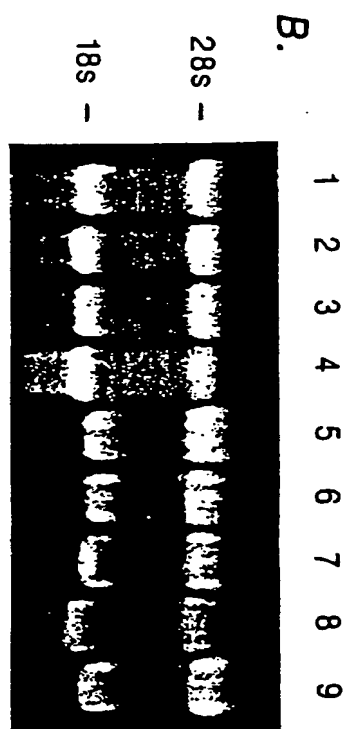


Fig. 17

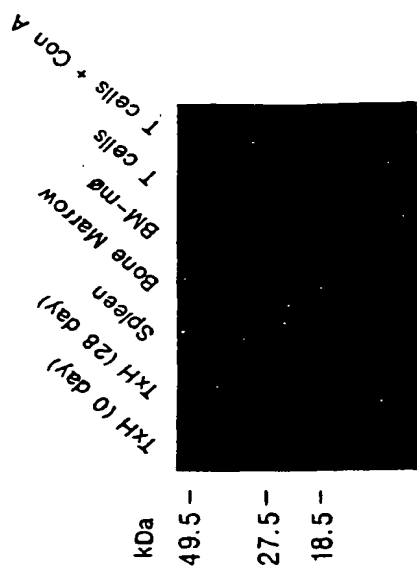


Fig. 18A

A

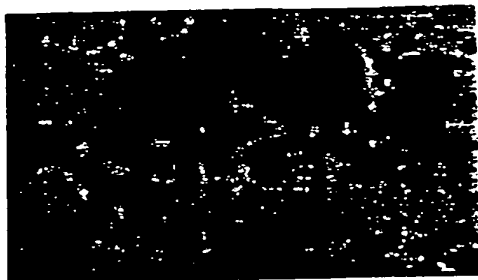


Fig. 18D

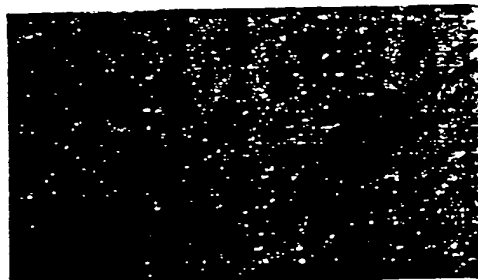


Fig. 18B

B



Fig. 18E



Fig. 18C

C

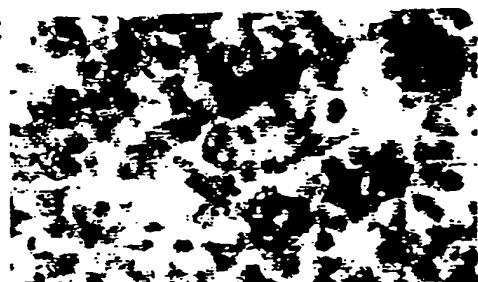
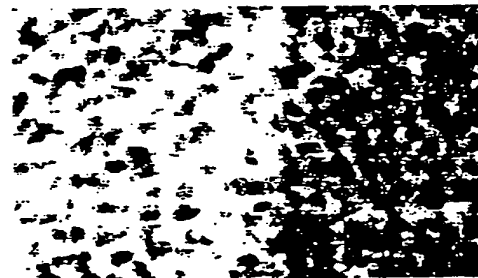
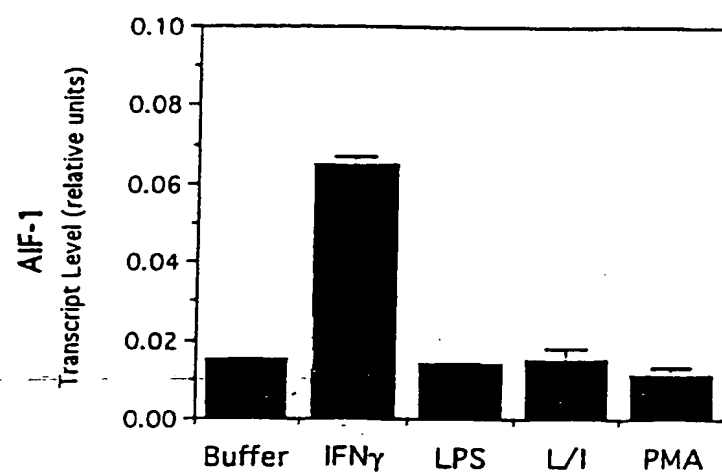


Fig. 18F





**A****FIG. 19A**

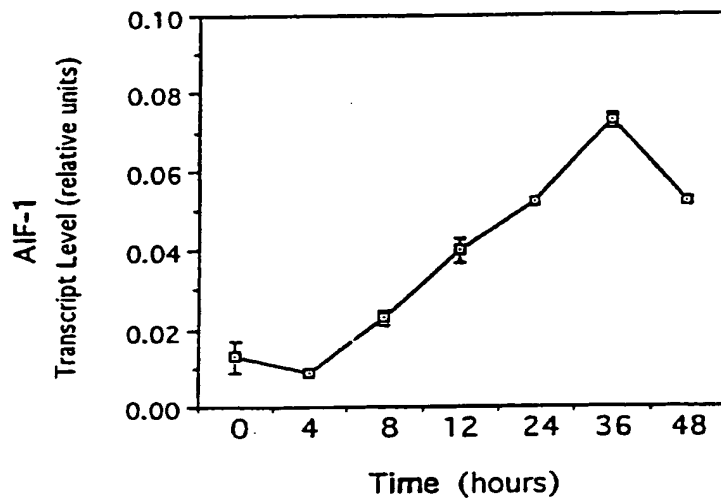
**B**

FIG. 19B

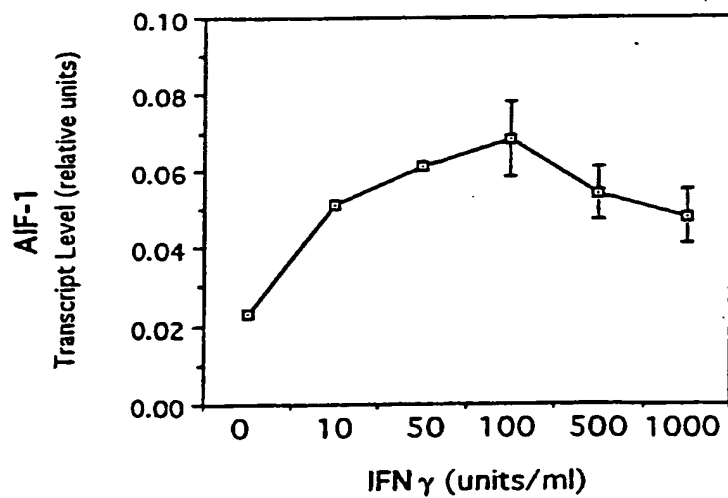
**C**

FIG. 19C

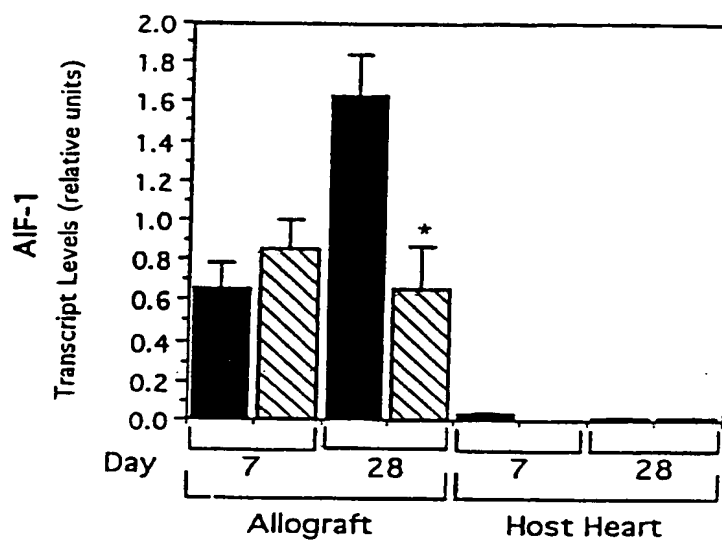
**A**

FIG. 20A

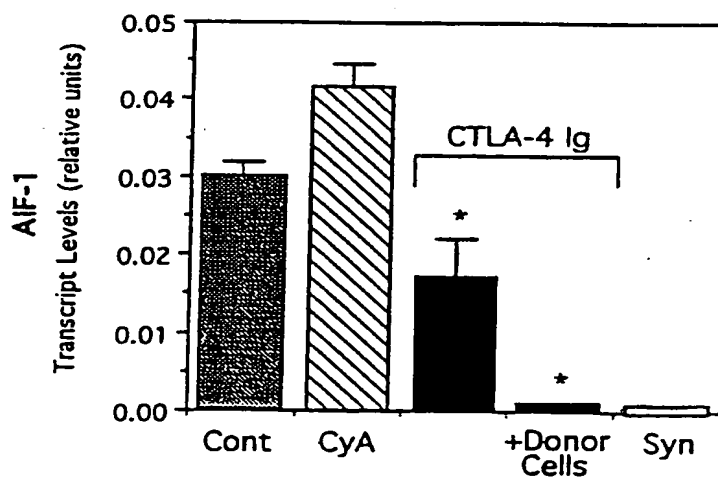
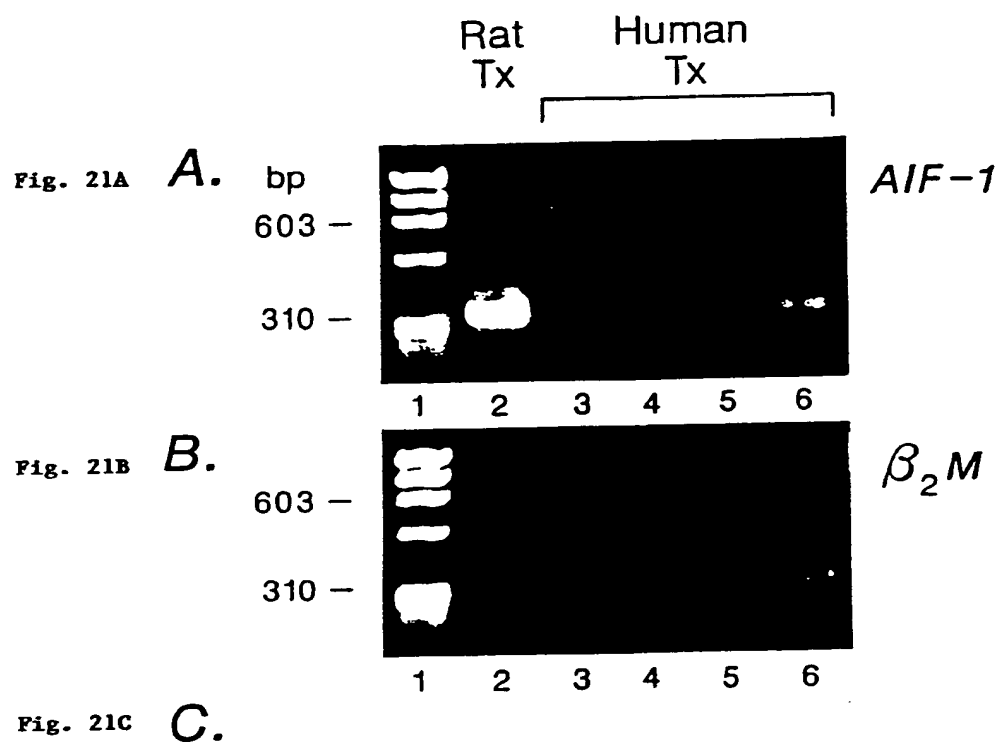
**B**

FIG. 20B



SEQ ID NO: 5 rAIF-1 MSQSKDLQGGKAFGLLKAQQEERLDGINKHFLDDPKYSSDEDLQSKLEAF 50  
|||.:.|||||:|||||:|||||:|||||:|  
SEQ ID NO: 42 hAIF-1 MSQTRDLQGGKAFGLLKAQQEERLDEINKQFLDDPKYSSDEDLPSKLEGF 50  
rAIF-1 KTKYMEFDLNGNGDIDIMSLKRMLEKLGVPKTHLELKKLIREVSSGSEET 100  
|.|||||:|||||:|||||:|||||:|  
hAIF-1 KEKYMEFDLNGNGDIDIMSLKRMLEKLGVPKTHLELKKLIGEVSSGSGET 100  
rAIF-1 FSYSDFLRMMLGKRSAILRMILMYEKNKEHQKPTGPPAKKAISELP 147  
|||.|||||:|||||:|.:.|||||  
hAIF-1 FSYPDFLRMMLGKRSAILKMILMYEEKAREKEKPTGPPAKKAISELP 147

FIG. 22

Fig. 23A

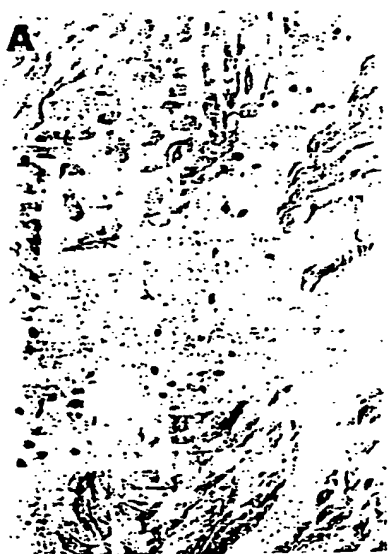


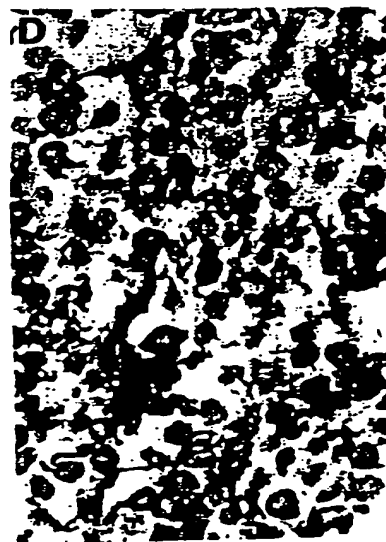
Fig. 23C



Fig. 23B



Fig. 23D



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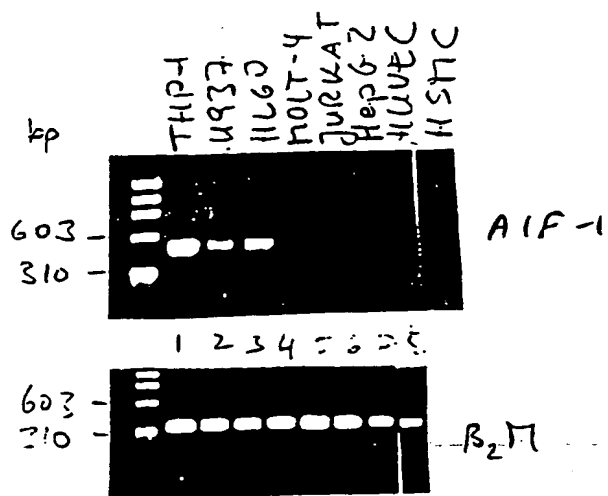


Fig. 24A

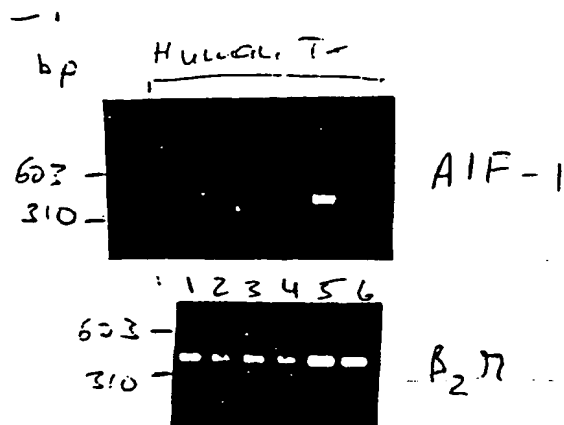


Fig. 24B

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US94/14724

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12N 15/00

US CL : 435/6, 172.3; 536/24.3, 24.31, 24.32, 24.33

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 172.3; 536/24.3, 24.31, 24.32, 24.33

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS and DIALOG (files 5, 155, 351, 357, 358) search terms: differential expression, transplant, rejection, allograft, syngraft, cardiac, cloning, PCR, polymerase chain reaction

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JOURNAL OF IMMUNOLOGY, Volume 148, No. 5, issued 01 March 1992, I. Papp et al, "Evidence for Functional Heterogeneity of Rat CD4 <sup>+</sup> T Cells in vivo", pages 1308-1314, see entire document.	1
X,P	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES USA, Volume 91, issued July 1994, U. Utans et al, "Chronic cardiac rejection: Identification of five upregulated genes in transplanted hearts by differential mRNA display", pages 6463-6467, see entire document.	1

☒ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

•	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"A"	document member of the same patent family

Date of the actual completion of the international search

07 FEBRUARY 1995

Date of mailing of the international search report

18 APR 1995

Name and mailing address of the ISA/US  
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Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

MARIANNE P. ALLEN

Telephone No. (703) 308-0196



## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US94/14724

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	NUCLEIC ACIDS RESEARCH, Volume 21, No. 14, issued 1993, P. Liang et al, "Distribution and cloning of eukaryotic mRNAs by means of differential display: refinements and optimization", pages 3269-3275, see entire document.	1
Y	NUCLEIC ACIDS RESEARCH, Volume 20, No. 19, issued 1992, J. Welsh et al, "Arbitrarily primed PCR fingerprinting of RNA", pages 4965-4970, see entire document.	1

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US94/14724

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US94/14724

## BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

- I. Claim 1, drawn to a method of identifying a gene which is differentially expressed in an allograft, classified in Class 435, subclass 6.
- II. Claims 2 and 14-16, drawn to a method of diagnosing allograft rejection, classified in Class 435, subclass 4.
- III. Claims 3-10, drawn to AIF-1 DNA and AIF-1 peptide, classified in at least Class 536, subclass 23.5, for example.
- IV. Claims 11-13, drawn to AIF-2 DNA and AIF-2 peptide, classified in at least Class 536, subclass 23.5, for example.
- V. Claims 17-21, drawn to a method of inhibiting rejection by inhibiting gene expression, classified in Class 514, subclass 44.
- VI. Claims 22-23, drawn to a method of identifying a compound capable of inhibiting allograft rejection, classified in Class 435, subclass 7.1.
- VII. Claim 24, drawn to an inhibitor, classified in at least Class 530, subclass 350, for example.
- VIII. Claim 25, drawn to a method of diagnosing inflammation in blood vessels, classified in at least Class 435, subclass 6, for example.
- IX. Claim 26, drawn to a method of inhibiting atherosclerosis, classified in at least Class 514, subclass 44, for example.

The inventions listed as Groups I-IX do not meet the requirements for Unity of Invention for the following reasons: The claims are not so linked by special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept. Group I forms the first appearing, single inventive concept. Groups I-II, V-VI, and VIII-IX are directed to distinct methods having different goals, method steps, and starting materials. Groups III-IV and VII are directed to structurally distinct compounds. It is noted that PCT Rule 13 does not provide for multiple products or methods within a single application.

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